

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 14:41:23 ; Search time 29.7961 Seconds

(without alignments)
1108.034 Million cell updates/sec

Title: US-09-224-683-46

Perfect score: 1061

Sequence: 1 MKKTQTWLTCIYLQLLFN.....AASLRNDSNSSNKYIYL 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1061	100.0	208	16 AAR83977	Human stem cell fa
2	1061	100.0	208	17 AAR83175	Stem cell factor.
3	1061	100.0	208	21 AAU53286	Human stem cell fa
4	1061	100.0	208	22 AAU53255	Human stem cell fa
5	1061	100.0	208	22 AAB83355	Human stem cell f
6	1061	100.0	208	22 AAU02457	Human SCF (stem ce
7	1061	100.0	208	22 AAU02764	Human SCF (stem ce
8	1061	100.0	208	22 AAB73565	Human SCF (stem ce
9	1061	100.0	208	22 AAB96940	Human stem cell fa

10	1061	100.0	208	23 AAB95641	Human SCF protein
11	1061	100.0	208	23 AAE22323	Human stem cell fa
12	1052	99.2	208	12 AAR11710	Human Stem Cell Fa
13	1030	97.1	273	12 AAR11711	Human Stem Cell Fa
14	1030	97.1	273	13 AAR20647	Human mast cell gr
15	1030	97.1	273	16 AAR83978	Human stem cell fa
16	1030	97.1	273	18 AAW27607	Human recombinant
17	1030	97.1	273	21 AAU53284	Human SCF protein
18	1030	97.1	273	22 AAU05256	Human stem cell fa
19	1030	97.1	273	22 AAU05266	Human SCF protein
20	1030	97.1	273	22 AAB98356	Human stem cell fa
21	1030	97.1	273	22 AAB98357	Human SCF protein
22	1030	97.1	273	22 AAB98367	Human SCF protein
23	1030	97.1	273	22 AAU02458	Human SCF (stem ce
24	1030	97.1	273	22 AAU02460	Human SCF protein
25	1030	97.1	273	22 AAU02765	Human SCF (stem ce
26	1030	97.1	273	22 AAU02766	Human SCF protein
27	1030	97.1	273	22 AAB73566	Human SCF (stem ce
28	1030	97.1	273	22 AAB73567	Human SCF protein
29	1030	97.1	273	22 AAB96941	Human stem cell fa
30	1030	97.1	273	22 AAB96942	Human stem cell fa
31	1030	97.1	273	22 AAB96952	Human stem cell fa
32	1030	97.1	273	23 AAB95642	Human SCF protein
33	1030	97.1	273	23 AAE22324	Human stem cell fa
34	1030	97.1	273	23 AAE22326	Human SCF protein
35	1026	96.7	273	22 AAU05257	Monkey stem cell f
36	1026	96.7	273	22 AAB98358	Monkey SCF protein
37	1026	96.7	273	22 AAU02484	Monkey SCF (stem c
38	1026	96.7	273	22 AAU02770	Monkey SCF (stem c
39	1026	96.7	273	22 AAB73571	Monkey SCF (stem c
40	1026	96.7	273	22 AAB96943	Monkey stem cell f
41	1021	96.2	273	14 AAR32166	hKL fragment A. S
42	1011	95.3	198	23 AAB95640	Human SCF protein
43	1001	94.3	196	22 AAU02456	Human SCF (stem ce
44	1001	94.3	196	22 AAU02763	Human SCF (stem ce
45	1001	94.3	196	22 AAB73564	Human SCF (stem ce

ALIGNMENTS

RESULT 1
AAR83977
ID AAR83977 standard; Protein; 208 AA.
XX AAR83977;
AC AAR83977;
XX
DT 25-MAR-2003 (updated)
DT 14-MAY-1996 (first entry)
XX
DE Human stem cell factor (SCF).
XX
XX Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW transplant; neoplasia; myelosuppression; bone marrow.
XX
XX Homo sapiens.
XX
XX Key
FH Peptide
FT
FT Protein
FT
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XX
PN EP676470-A1.
XX
PD 11-OCT-1995.
XX
XX
PF 04-OCT-1990; 9SEP-0105391.
XX
XX 01-OCT-1990; 9OUS-0589701.
PR 16-OCT-1989; 89US-0422383.
PR 11-JUN-1990; 9OUS-0537198.

24-AUG-1990; 90US-0573616.
PR 28-SEP-1990; 90MO-US05548.
XX
PA (AMGEN -) AMGEN INC.
X1 Bosselman RA, Martin FH, Suggs SV, Zsebo KM;
X2 WPI, 1995-346090/45.
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[illegible]

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FT		/label= Mat_protein	
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XX	WO9614410-A1.		
XX			
PD	17-MAY-1996.		
XX			
PE	31-OCT-1995;	95WO-GB02547.	
XX			
XX	28-APR-1995;	95GB-0008618.	
PR	04-NOV-1994;	94GB-0022293.	
XX			
PA	(ISUF) ARS APPLIED RES SYST HOLDING NV.		
XX			
PI	Dellow KA, Sharkey AM, Smith SK;		
XX			
DR	WPI; 1996-251760/25.		
DR	N-PSDB; AAT29489.		
XX			
PT	Stem cell factor comprising C-terminal sequence given in		
PT	specification - useful to ensure correct development of		
PT	pre-implantation embryos before implantation into subject		
XX			
PS	Disclosure; Fig 2; 25pp; English.		
XX			
CC	A DNA sequence (AAT29489) codes for human stem cell factor (SCF).		
CC	(AAR95175). The full-length SCF transcript consists of 8 exons.		
CC	A novel splice variant has been identified that appears to arise		
CC	from the inclusion of a novel exon (see also AAT29488) between exons		
CC	3 and 4 of the gene. The resulting frameshift produces a novel		
CC	SCF consisting of the first 39 amino acids of mature SCF followed		
CC	by a 33-amino acid C-terminal region (AAR95174). The novel SCF is		
CC	useful for ensuring correct development of pre-implantation embryos.		
XX			
XX			
SQ	Sequence	208 AA;	
Query Match		100.0%; Score 1061; DB 17; Length 208;	
Best Local Similarity		100.0%; Pred. NO. 4.8e-104; Indels	
Matches 208; Conservative		0; Mismatches	0; Gaps
			0

Query Match	Similarity	Score	IDB	Length
Best Local	100.0%	1061	DB 17	208
Matches	208	Conservative	100.0%	Pred. No. 4.8e-104
		Mismatches	0	Indels
		Gaps	0	

Query	Match	Similarity	Score	IDB	Length
Db	1	MKTQTMILTCIYVQLLFNPLVTEGICRRRVNNVVDYTKLVANLPKDMITLKYVPG	60		
Db	1	MKTQTMILTCIYVQLLFNPLVTEGICRRRVNNVVDYTKLVANLPKDMITLKYVPG	60		
Qy	61	MDVLPSCWISSEWVQJSDSLTDLLDKFNSISEGLSNYSIIDKLVINIVDDLVECKENSS	120		
Db	61	MDVLPSCWISSEWVQJSDSLTDLLDKFNSISEGLSNYSIIDKLVINIVDDLVECKENSS	120		
Qy	121	KDLKSKRSKSPPRPLFTPEEFRIINRSIDAFKDVVASSETSDCVVSSTLSPEKOSRVST	180		
Db	121	KDLKSKRSKSPPRPLFTPEEFRIINRSIDAFKDVVASSETSDCVVSSTLSPEKOSRVST	180		
Qy	181	KPFMLPVAASLSLNDSSSSNSKTIYLI	208		
Db	181	KPFMLPVAASLSLNDSSSSNSKTIYLI	208		

RESULT 3	ID	AA
AA53286	AA53286	standard; Protein: 208 AA.
AA53286	AA53286	
XX	XX	27-JUL-2000 (first entry)
XX	XX	Human stem cell factor protein sequence.
XX	XX	Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
XX	XX	primitive progenitor cell; haematopoietic disorder; syngenic;
XX	XX	allogeneic; autologous bone marrow transplant; gene therapy;
XX	XX	transfection; haematopoietic stem cell; acute blood loss; neoplasia;
XX	XX	cancer.

OS Homo sapiens.
 XX
 PN EP92579-A1.
 XX
 PD 12-APR-2000.
 XX
 PF 04-OCT-1990; 99EP-0122861.
 XX
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 28-SEP-1990; 90MO-US05548.
 PR 01-OCT-1990; 90US-0589701.
 PR 04-OCT-1990; 90EP-0310899.
 XX
 PA (AMGE-) AMGEN INC.
 PI Zsebo KM, Suggs SV, BosseImann RA, Martin FH;
 DR WPI; 2000-259135/23.
 DR N-PSDB; AAA13716.
 XX
 PT Production of hematopoietic cells suitable for administration to a
 PT subject using progenitor cells and expanding the cells using stem cell
 PT factor -
 XX
 PS Claim 21; Fig 15C; 123pp; English.
 XX
 CC A method has been developed of making haematopoietic cells suitable for
 CC administration to a subject. The method comprises: (a) obtaining
 CC haematopoietic progenitor cells from a donor; and (b) expanding the
 CC cells by adding to the cells a haematopoietically effective dose of a
 CC polypeptide product having at least part of the primary structural
 CC confirmation and one or more of the biological properties of naturally
 CC occurring stem cell factor (SCF). The method is useful for stimulating
 CC primitive progenitor cells including early haematopoietic progenitor
 CC cells which are capable of maturing to erythroid, megakaryocyte,
 CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
 CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
 CC SCF is useful for treating haematopoietic disorders. The method is
 CC useful for expanding early haematopoietic progenitors in syngeneic,
 CC allogeneic or autologous bone marrow transplant. SCF is useful for
 CC enhancing the efficiency of gene therapy based on transfecting
 CC haematopoietic stem cells. SCF is also useful for combating the
 CC myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing
 CC haematopoietic recovery after acute blood loss and as a boost to the
 CC immune system for fighting neoplasia (cancer). The present sequence
 CC represents a specifically claimed human SCF from the present invention.
 XX
 SO Sequence 208 AA;

AAU05255
 ID AAU05255 standard; Protein; 208 AA.
 XX
 AC AAU05255;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human stem cell factor (SCF) protein encoded by SCF cDNA.
 XX
 KW Human; stem cell factor; SCF; haematopoietic progenitor cell;
 KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
 KW hypopigmentation disorder; viral disorder; AIDS.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /label= Signal_peptide
 FT Protein 26..208
 FT /label= Mature_SCF
 XX
 PN US6248319-B1.
 XX
 PD 19-JUN-2001.
 XX
 PF 24-MAY-1995; 95US-0449653.
 XX
 PR 10-APR-1991; 91US-0684535.
 PR 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 PR 21-DEC-1993; 93US-0172329.
 XX
 PA (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSELMAN R A.
 PA (SUGS/) SUGGS S V.
 PA (MART/) MARTIN F H.
 PI Zsebo KM, BosseImann RA, Suggs SV, Martin FH;
 DR WPI; 2001-407312/43.
 DR N-PSDB; AAS10457.
 XX
 PT Increasing the number of early haematopoietic progenitor cells in the
 PT peripheral blood useful for the treatment of blood disorders including
 PT Hodgkin's disease comprises the administration of human stem cell
 PT factor -
 XX
 PS Example 3; Fig 15C; 210pp; English.
 XX
 CC The present sequence represents human stem cell factor (SCF). The
 CC sequence is described in an invention relating to novel stem cell
 CC factors, the polynucleotides encoding them and methods for producing
 CC the stem cell factors. The methods involve increasing the number of
 CC early haematopoietic progenitor cells in human peripheral blood by
 CC administering a haematopoietically effective human stem cell factor
 CC polypeptide. The methods are useful for the treatment of blood
 CC disorders, including myelofibrosis, myelocytosis, osteopetrosis,
 CC metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's
 CC disease, lymphoma, Gaucher's disease, Niemann-Pick disease, refractory
 CC anaemia, malaria, vitamin B12 and folic acid deficiency,
 CC hypopigmentation disorders i.e. prebaldism and viral induced disorders,
 CC including AIDS.
 XX
 SO Sequence 208 AA;

Query Match 100.0%; Score 1061; DB 22; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4.8e-104;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLQLLFNPLVKTEGICRNVTNNVDVTLVANLPKDWITLKYVVG 60

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Db      1 MKKTQWTLITLCIYQLLLFNPVLVKTGICRRNRYTNVADVTKLVANLPKDYMITLKYPG 60
QY      61 MDVLPSCWISSEWVQVLSLTDLDKPSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120
Db      61 MDVLPSCWISSEWVQVLSLTDLDKPSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120
QY      121 KDLKSFSPSPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
Db      121 KDLKSFSPSPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
QY      181 KPFLMPVVAASLRNDSSSSNSKYYILI 208
Db      181 KPFLMPVVAASLRNDSSSSNSKYYILI 208

RESULT 5
AAB98355
ID      AAB98355 standard; Protein; 208 AA.
AC      AAB98355;
XX
XX      21-AUG-2001 (first entry)
DE      Human stem cell factor (SCF) protein SEQ ID NO:46.
XX
XX      Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
XX      gene therapy.
XX      Homo sapiens.
XX      US6207454-B1.
XX      27-MAR-2001.
XX      31-DEC-1998; 98US-0224681.
XX
XX      21-DEC-1993; 93US-0172329.
XX      24-MAY-1995; 95US-0449653.
XX      12-JUN-1998; 98US-0005893.
XX      25-NOV-1992; 92US-0982255.
XX      16-OCT-1989; 89US-0422383.
XX      11-JUN-1990; 90US-0537198.
XX      24-AUG-1990; 90US-0573616.
XX      01-OCT-1990; 90US-0589701.
XX
XX      (AMGE-) AMGEN INC.
XX
XX      Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX      WPI; 2001-366062/38.
XX      N-PSDB; AAH41341.
XX
XX      Enhancing efficiency of transfer of polynucleotide into a target
XX      mammalian cell in vitro, involves exposing cell that expresses a stem
XX      cell factor receptor to stem cell factor, and introducing
XX      polynucleotide into cell in vitro -
XX
XX      Claim 16; Fig 15C; 210pp; English.
XX
XX      The present invention describes a method for enhancing (B) the
XX      efficiency of transfer of a polynucleotide (I) into a target mammalian
XX      cell (II) in vitro, comprising exposing (II) that expresses a stem cell
XX      factor (SCF) receptor to a biologically active SCF, its analogue or
XX      fragment, which induces cell proliferation, and introducing (I) to (II)
XX      in vitro. Exposure of SCF to (II) results in increased uptake of (I)
XX      into the cell. The method is useful for enhancing the efficiency of the
XX      transfer of a polynucleotide into a target mammalian cell in vitro.
XX      The method is useful in gene therapy techniques. AAH41301 to AAH41364
XX      and AAB98351 to AAB98390 represent sequences used in the exemplification
XX      of the present invention.
XX
XX      Sequence 208 AA:

```

```

Query Match      100.0%; Score 1061; DB 22; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.8e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKKTQWTLITLCIYQLLLFNPVLVKTGICRRNRYTNVADVTKLVANLPKDYMITLKYPG 60
Db      1 MKKTQWTLITLCIYQLLLFNPVLVKTGICRRNRYTNVADVTKLVANLPKDYMITLKYPG 60
QY      61 MDVLPSCWISSEWVQVLSLTDLDKPSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120
Db      61 MDVLPSCWISSEWVQVLSLTDLDKPSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120
QY      121 KDLKSFSPSPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
Db      121 KDLKSFSPSPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
QY      181 KPFLMPVVAASLRNDSSSSNSKYYILI 208
Db      181 KPFLMPVVAASLRNDSSSSNSKYYILI 208

RESULT 6
AAU02457
ID      AAU02457 standard; Protein; 208 AA.
XX
XX      AAU02457;
XX
XX      29-AUG-2001 (first entry)
DE      Human SCF (stem cell factor) protein encoded by SCF cDNA.
XX
XX      Human; stem cell factor; SCF; early haematopoietic progenitor cell;
XX      blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
XX      anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder.
XX      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      FH      Peptide      1..25
XX      FT      /label= Signal_peptide
XX      FT      Protein      26..208
XX      FT      /label= Mature_SCF
XX
XX      US6207417-B1.
XX
XX      27-MAR-2001.
XX
XX      07-JUN-1995; 95US-0482918.
XX
XX      21-DEC-1993; 93US-0172329.
XX      16-OCT-1989; 89US-0422383.
XX      11-JUN-1990; 90US-0537198.
XX      24-AUG-1990; 90US-0573616.
XX      01-OCT-1990; 90US-0589701.
XX
XX      (ZSEB/) ZSEBO K M.
XX      (BOSS/) BOSSSELMAN R A.
XX      (SUGG/) SUGGS S V.
XX      (MART/) MARTIN F H.
XX
XX      Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX      WPI; 2001-298941/31.
XX      N-PSDB; AAS04121.
XX
XX      Novel nucleic acids encoding stem cell factor useful for treating
XX      disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's
XX      disease, Kala azar, anaemia and septicemia -
XX      Example 3; Fig 15C; 209pp; English.
XX
XX      The present sequence represents human SCF (stem cell factor) protein

```


CC encoded by SCF cDNA. The present invention relates to novel stem cell
 CC factors (AAU02453-AAU02458, AAU02460, AAU02461) and the polynucleotides
 CC encoding them. SCF stimulate primitive progenitor cells including early
 CC haematopoietic progenitor cells. The invention also describes SCF
 CC peptides (AAU02462-AAU02481) and the oligonucleotides
 CC (AAU04081-AAU04117) used in the isolation of human and rat SCF
 CC sequences. The polynucleotide encoding SCF is useful for producing
 CC SCF and useful in gene therapy. It is useful for treating disorders
 CC involving blood cells such as myelofibrosis, metastatic carcinoma,
 CC acute leukemia, multiple myeloma, Hodgkin's disease, lymphoma,
 CC Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
 CC sarcoidosis, military tuberculosis, disseminated fungus disease,
 CC fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
 CC pyridoxine deficiency, and hypopigmentation disorders such as
 CC piebaldism and vitiligo.

XX Sequence 208 AA;

Query Match 100.0%; Score 1061; DB 22; Length 208;

Best Local Similarity 100.0%; Pred. No. 4.8e-104;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYPG 60

DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYPG 60

QY 61 MDVLPSCWISSEWVQLSDSLDLDKFSNISSEGLSNYSIIDLVNIYVDLVECKENSS 120

DB 61 MDVLPSCWISSEWVQLSDSLDLDKFSNISSEGLSNYSIIDLVNIYVDLVECKENSS 120

QY 121 KDLKSFSPKPEPRLTPPEPFRIFNRSIDAFKDFVVASETSDCVSVSTLSPKDSRVSVT 180

DB 121 KDLKSFSPKPEPRLTPPEPFRIFNRSIDAFKDFVVASETSDCVSVSTLSPKDSRVSVT 180

QY 181 KPFMLPPVAASGLRNDSSSSNSKYIYL 208

DB 181 KPFMLPPVAASGLRNDSSSSNSKYIYL 208

RESULT 7

AAU02764 ID AAU02764 standard; Protein; 208 AA.

XX AAU02764;

AC 29-AUG-2001 (first entry)

XX Human SCF (stem cell factor) protein encoded by SCF cDNA.

XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;

XX blood disorder; leukemia; Hodgkin's disease; lymphoma; splenomegaly;

XX anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25 /label= Signal_peptide

FT Protein 26..208 /label= Mature_SCF

XX US6218148-B1.

XX 17-APR-2001.

XX 21-DEC-1993; 93US-0172329.

XX 25-NOV-1992; 92US-0982255.

XX 16-OCT-1989; 89US-0422383.

XX 11-JUN-1990; 90US-0537198.

XX 24-AUG-1990; 90US-0573616.

XX 01-OCT-1990; 90US-0589701.

PA (AMGE-) AMGEN INC.

XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

PI WPI; 2001-281051/29.

DR N-PSDB; AAS04222.

XX Example 3; Fig 15C; 167bp; English.

PS The present sequence represents human SCF (stem cell factor) protein

CC encoded by SCF cDNA. The present invention relates to novel stem cell

CC factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797) and the

CC polynucleotides encoding them. SCF stimulate primitive progenitor cells

CC including early haematopoietic progenitor cells. The invention also

CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides

CC (AAU04182-AAU04218) used in the isolation of human and rat SCF

CC sequences. The polynucleotide encoding SCF is useful for producing

CC SCF and useful in gene therapy. It is useful for treating disorders

CC involving blood cells such as myelofibrosis, metastatic carcinoma,

CC acute leukemia, multiple myeloma, Hodgkin's disease, lymphoma,

CC Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,

CC sarcoidosis, military tuberculosis, disseminated fungus disease,

CC fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,

CC pyridoxine deficiency, and hypopigmentation disorders such as

CC piebaldism and vitiligo.

XX Sequence 208 AA;

QY Query Match 100.0%; Score 1061; DB 22; Length 208;

DB Best Local Similarity 100.0%; Pred. No. 4.8e-104; Indels 0; Gaps 0;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYPG 60

DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYPG 60

QY 61 MDVLPSCWISSEWVQLSDSLDLDKFSNISSEGLSNYSIIDLVNIYVDLVECKENSS 120

DB 61 MDVLPSCWISSEWVQLSDSLDLDKFSNISSEGLSNYSIIDLVNIYVDLVECKENSS 120

QY 121 KDLKSFSPKPEPRLTPPEPFRIFNRSIDAFKDFVVASETSDCVSVSTLSPKDSRVSVT 180

DB 121 KDLKSFSPKPEPRLTPPEPFRIFNRSIDAFKDFVVASETSDCVSVSTLSPKDSRVSVT 180

QY 181 KPFMLPPVAASGLRNDSSSSNSKYIYL 208

DB 181 KPFMLPPVAASGLRNDSSSSNSKYIYL 208

RESULT 8

AAU03565 ID AAU03565 standard; Protein; 208 AA.

XX AAU03565;

AC 07-AUG-2001 (first entry)

XX Human SCF (stem cell factor) protein #2, encoded by SCF cDNA.

XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;

XX blood disorder; leukemia; Hodgkin's disease; lymphoma; splenomegaly;

XX anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25 /label= Signal_peptide

FT Protein 26..208 /label= Mature_SCF

XX XX US6204363-B1.
XX XX 20-MAR-2001.
XX XX 25-NOV-1992; 92US-0982255.
XX XX 10-APR-1991; 91US-0684535.
XX XX 16-OCT-1989; 89US-0422383.
XX XX 11-JUN-1990; 90US-0537198.
XX XX 24-AUG-1990; 90US-0573616.
XX XX 01-OCT-1990; 90US-0589701.
XX XX (AMGE-) AMGEN INC.
XX XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX XX WPI; 2001-256683/26.
XX XX N-PSDB; AAB23899.
XX XX
XX XX New stem cell factor polypeptides and their analogs which stimulate
XX XX growth of early hematopoietic progenitors, useful for treating aplastic
XX XX anemia, carcinoma, multiple myeloma, vitiligo, Kala azar, Hodgkin's
XX XX disease -
XX XX Claim 1; Fig 15C; 166pp; English.
XX XX
XX XX The present sequence represents human SCF (stem cell factor) protein
XX XX encoded by SCF cDNA. The present invention relates to novel stem cell
XX XX factors (AAB73561-AAB73568, AAB73571-AAB73576) and the
XX XX polynucleotides encoding them. SCF stimulate primitive progenitor cells
XX XX including early hematopoietic progenitor cells. The invention also
XX XX describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides
XX XX (AAH23859-AAH23895) used in the isolation of human and rat SCF
XX XX sequences. The polynucleotide encoding SCF is useful for producing
XX XX SCF and useful in gene therapy. It is useful for treating disorders
XX XX involving blood cells such as myelofibrosis, metastatic carcinoma,
XX XX acute leukemia, multiple myeloma, Hodgkin's disease, lymphoma,
XX XX Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
XX XX sarcoidosis, military tuberculosis, disseminated fungus disease,
XX XX Fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
XX XX pyridoxine deficiency, and hypopigmentation disorders such as
XX XX piebaldism and vitiligo.
XX XX
XX XX Sequence 208 AA;
XX XX
XX XX Query Match 100.0%; Score 1061; DB 22; Length 208;
XX XX Best Local Similarity 100.0%; Pred. No. 4,8e-104;
XX XX Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISEMNVQVLSLTDLDKFSNISSEGLSNYSIIDLVNIYVDLVECKENSS 120
DB 61 MDVLPSCWISEMNVQVLSLTDLDKFSNISSEGLSNYSIIDLVNIYVDLVECKENSS 120
QY 121 KDLKSFKSPPEPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
DB 121 KDLKSFKSPPEPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
QY 181 KPFLMPVVAASLNRDSSSSNKYIYLI 208
DB 181 KPFLMPVVAASLNRDSSSSNKYIYLI 208
RESULT 9
AAB96940
ID AAB96940 standard; Protein; 208 AA.
XX AAB96940;
XX AC
XX XX

DT 13-JUL-2001 (first entry)
XX XX
XX XX Human stem cell factor SEQ ID NO: 46.
XX XX
XX XX Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
XX XX gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
XX XX neurological damage; intestinal damage; infertility; AIDS; SCID;
XX XX severe combined immunodeficiency.
XX XX Homo sapiens.
XX XX
XX XX Key Location/Qualifiers
XX XX FT Peptide 1..25
XX XX FT /label= signal_peptide
XX XX FT Protein 26..208
XX XX FT /label= mature_stem_cell_factor
XX XX
XX XX US6207802-B1.
XX XX 27-MAR-2001.
XX XX
XX XX 09-NOV-1994; 94US-0336728.
XX XX
XX XX 25-NOV-1992; 92US-0982255.
XX XX 16-OCT-1989; 89US-0422383.
XX XX 11-JUN-1990; 90US-0537198.
XX XX 24-AUG-1990; 90US-0573616.
XX XX 01-OCT-1990; 90US-0589701.
XX XX (AMGE-) AMGEN INC.
XX XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX XX WPI; 2001-353108/37.
XX XX N-PSDB; AAB89101.
XX XX
XX XX Novel isolated non-human mammalian stem cell factor polypeptide
XX XX stimulating growth of early haematopoietic progenitor cells, useful for
XX XX treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,
XX XX sarcooidosis -
XX XX Disclosure; Fig 15C; 209pp; English.
XX XX
XX XX The present invention provides the protein and coding sequences of
XX XX mammalian stem cell factors (SCFs). These are capable of stimulating the
XX XX growth of early haematopoietic progenitor cells, neural stem cells and
XX XX primordial germ stem cells. The sequences are useful in the treatment of
XX XX leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
XX XX nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
XX XX immunodeficiency (SCID). The present sequence is an SCF described in the
XX XX invention.
XX XX
XX XX Sequence 208 AA;
XX XX
XX XX Query Match 100.0%; Score 1061; DB 22; Length 208;
XX XX Best Local Similarity 100.0%; Pred. No. 4,8e-104;
XX XX Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISEMNVQVLSLTDLDKFSNISSEGLSNYSIIDLVNIYVDLVECKENSS 120
DB 61 MDVLPSCWISEMNVQVLSLTDLDKFSNISSEGLSNYSIIDLVNIYVDLVECKENSS 120
QY 121 KDLKSFKSPPEPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
DB 121 KDLKSFKSPPEPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
QY 181 KPFLMPVVAASLNRDSSSSNKYIYLI 208
DB 181 KPFLMPVVAASLNRDSSSSNKYIYLI 208

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Db      181 KPFLMPVAASLRNDSSSNKITYILI 208
RESULT 10
ID      ABG95641
ABG95641 standard; Protein; 208 AA.
XX
XX      ABG95641;
AC
XX
XX      05-DEC-2002 (first entry)
DE
XX
XX      Human SCF protein sequence encoded by cDNA.
KW
XX      Stem cell factor; SCF; blood-forming system; blood cell disorder;
KW      haematopoietic system; metastatic carcinoma; acute leukaemia;
KW      multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
KW      refractory erythroblastic anaemia; military tuberculosis; cytostatic;
KW      disseminated fungus disease; haematopoietic; tuberculous;
KW      antianemic; antifungal; antimalarial; dermatological; human.
XX
XX      Homo sapiens.
OS
XX
XX      EP1241258-A2.
PN
XX
XX      18-SEP-2002.
PD
XX
XX      04-OCT-1990; 2002EP-0008587.
PF
XX
XX      16-OCT-1989; 89US-0422383.
PR      11-JUN-1990; 90US-0537198.
PR      24-AUG-1990; 90US-0573616.
PR      28-SEP-1990; 90MO-US05548.
PR      01-OCT-1990; 90US-0589701.
PR      04-OCT-1990; 90EP-0310899.
PR      04-OCT-1990; 95EP-0105391.
XX
XX      (AMGE-) AMGEN INC.
PA
XX
XX      Zsebo KM, Suggs SV, Bosselman RA, Martin FH;
PI
XX      WPI; 2002-684093/74.
DR      N-PSDB; ABS73858.
XX
XX      Production of a human stem cell factor (SCF) polypeptide for treating
PT      disorders involving blood cells, such as leukaemia, comprises culturing
PT      mammalian cells comprising non-human SCF promoter DNA linked to DNA
PT      encoding the human SCF
XX
XX      Claim 1; Fig 15C; 120pp; English.
PS
XX
XX      The present invention relates to novel stem cell factors (SCFs),
XX      polynucleotide sequences encoding the SCFs, and methods of producing
XX      them. SCFs are involved in the blood-forming (haematopoietic)
XX      system in mammals, particularly humans. The method of the invention
XX      is useful for the production of human SCF. The stem cell factors are
XX      useful to treat disorders involving blood cells e.g. metastatic
XX      carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
XX      lymphoma, refractory erythroblastic anaemia, military tuberculosis,
XX      disseminated fungus disease, malaria, and vitiligo. The present
XX      sequence represents human SCF protein.
SQ
XX
XX      Sequence 208 AA;
Query Match 100.0%; Score 1061; DB 23; Length 208;
Best Local Similarity 100.0%; Pred. No. 4, 8e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY      1 MKKTQTMTTCIYTLQLLFNPFLVKTGICGRNVTNNVVKDYTKLVANLPKDYMTLTKVPG 60
OY      1 MKKTQWMTTCIYTLQLLFNPFLVKTGICGRNVTNNVVKDYTKLVANLPKDYMTLTKVPG 60
OY      61 MDVLPSEHCNISSEWVQLSDSLTDLDFKSNISGCLSNYSGLTIDKLVNIIVDDIVCEKENS 120

```

Db	61	MDVLPEHCIMSEMVQGLSDSLDLDLDRKSNISSEGLSNYSIIIDKLWNIVDDLVEQVENS	12
Oy	121	KDIKKSFKSPERPLFTPEEFERRINRSIDAFKDFVVASETSDCVSSTLSPEKORSVVT	180
Db	121	KDIKKSFKSPERPLFTPEEFERRINRSIDAFKDFVVASETSDCVSSTLSPEKORSVVT	180
Oy	181	KPFWLPPVAASSLRDSSSSNKTYLYI	208
Db	181	KPFWLPPVAASSLRDSSSSNKTYLYI	208
RESULT 11			
ID	AAE2323	standard; Protein, 208 AA.	
AC	AAE2323;		
DT	25-JUL-2002	(first entry)	
DE	Human stem cell factor (SCF) protein #2.		
XX	Human; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;		
XX	anemia; myelosuppression; nerve damage; myeloproliferative disorder;		
XX	infertility; neoplasia; myelofibrosis; myelocytosis; osteoporosis;		
XX	metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;		
XX	Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;		
XX	Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;		
XX	Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;		
XX	disseminated fungus disease; Pulmonary septicaemia; plebaldism; AIDS;		
XX	acquired immune deficiency syndrome; malaria; military tuberculosis;		
XX	pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;		
XX	Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo.		
OS	Homo sapiens.		
PH	Key	Location/Qualifiers	
FT	Peptide	1..25	
FT	Protein	/label= Signal-peptide	
FT		26..208	
FT		/note= "Human mature SCF protein"	
XX	US2002018763-A1.		
PD	14-FEB-2002.		
PF	12-JAN-1998;	98US-0005243.	
XX	24-MAY-1995;	95US-0449653.	
PR	(ZSEB/) ZSEBO R M.		
PA	(BOSS/) BOSSELMAN R A.		
PA	(SUGG/) SUGGS S V.		
XX	(MART/) MARTIN F H.		
PI	Zsebo KM, Bosseelman RA, Suggs SV, Martin FH,		
XX	WPI; 2002-350789/38.		
DR	N-PSDB; AAD35474.		
XX	Novel non-naturally-occurring stem cell factor polypeptide, useful for		
PT	treating leucopenia, thrombocytopenia, anemia and for enhancing		
XX	engraftment of bone marrow during transplantation in a mammal -		
PS	Claim 9; Fig 15C; 217pp; English.		
CC	The present invention relates to novel non-naturally-occurring stem cell		
CC	factor (SCF) polypeptides having an amino acid sequence sufficiently		
CC	duplicative of that of naturally-occurring SCF to allow possession of		
CC	haematopoietic biological activity of naturally occurring SCF. Sequences		
CC	of the invention are useful for treating leucopaenia, thrombocytopaenia,		
CC	anaemia and for enhancing bone marrow recovery in treatment of radiation,		
CC	engraftment of bone marrow during transplantation in mammals and chemical		
CC	or chemotherapeutic induced bone marrow aplasia or myelosuppression. They		

CC are also useful for treating acquired immune deficiency in a human, nerve
 CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal
 CC damage in a mammal. SCF sequences are useful for preparing biologically
 CC active polymer polypeptide adduct, for enhancing transfection of early
 CC hematopoietic progenitor cells with a gene, and transfer of a gene into
 CC a mammal. They are useful for treating myelofibrosis, myelocytosis,
 CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
 CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
 CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
 CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
 CC splenic pancytopenia, disseminated fungus disease, malaria, military
 CC tuberculosis, fulminating septicaemia, pyridoxine deficiency, vitamin
 CC B12 and follic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
 CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)
 CC and vitiligo. The present sequence is human SCF protein.

XX Sequence 208 AA;

SO Query Match 100.0%; Score 1061; DB 23; Length 208;

Best Local Similarity 100.0%; Pred. No. 4.8e-104;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLFNPLVKTGICRRVYTNVNDVTKLVANLPKDYMITLKYPVG 60
 DB 1 MKKTQWTLTCTIYQLLFNPLVKTGICRRVYTNVNDVTKLVANLPKDYMITLKYPVG 60
 QY 61 MDVLPSCWISEMNVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVCEKENS 120
 DB 61 MDVLPSCWISEMNVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVCEKENS 120
 QY 121 KDLKSFKSPPEPRLTPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
 DB 121 KDLKSFKSPPEPRLTPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
 QY 181 KPFLMPVVAASSLRNDSSSSNSKTYITL 208
 DB 181 KPFLMPVVAASSLRNDSSSSNSKTYITL 208

RESULT 12

ID AAR11710 standard; Protein; 208 AA.

AC AAR11710;

DT 20-JUN-1991 (first entry)

DE Human Stem Cell Factor.

KW Stem cell factor; SCF; leukopenia; AIDS; haematopoiesis.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25

FT Protein /label= sig_peptide

FT Protein /label= mat_protein

PN EP423980-A.

PD 24-APR-1991.

XX 04-OCT-1990; 90EP-0310899.

XX 01-OCT-1990; 90US-0589701.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 28-SEP-1990; 90MO-US05548.

XX (AMGE-) AMGEN INC.

PI Zsebo KM, Suggs SV, Bosseman RA, Martin FH;

XX WPI; 1991-119233/17.

DR N-PSDB; AAQ11540, AAQ11541.

XX New naturally-occurring polypeptide stem cell factor analogues -

PT have hematopoietic biological activity of stem cell factor and

PT are used to treat eg leukopenia, AIDS, nerve damage and

PT infertility

XX Disclosure; Fig 15C; 127pp; English.

XX The SCF has the ability to stimulate growth of primitive

CC progenitors including early hematopoietic progenitor cells and non-

CC hematopoietic stem cells such as neural stem cells and primordial

CC germ stem cells. The product may be used in a pharmaceutical

CC compsn. for treating, in a mammal, leukopenia, thrombocytopenia,

CC anaemia, AIDS, neoplasia, nerve damage, infertility and

CC intestinal damage.

CC See also AAR11708, AAQ11509-Q11543.

XX Sequence 208 AA;

SO Query Match 99.2%; Score 1052; DB 12; Length 208;

Best Local Similarity 99.5%; Pred. No. 4.3e-103;

Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLFNPLVKTGICRRVYTNVNDVTKLVANLPKDYMITLKYPVG 60

DB 1 MKKTQWTLTCTIYQLLFNPLVKTGICRRVYTNVNDVTKLVANLPKDYMITLKYPVG 60

QY 61 MDVLPSCWISEMNVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVCEKENS 120

DB 61 MDVLPSCWISEMNVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVCEKENS 120

QY 121 KDLKSFKSPPEPRLTPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180

DB 121 KDLKSFKSPPEPRLTPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180

QY 181 KPFLMPVVAASSLRNDSSSSNSKTYITL 208

DB 181 KPFLMPVVAASSLRNDSSSSNSKTYITL 208

RESULT 13

ID AAR11711 standard; Protein; 273 AA.

AC AAR11711;

DT 20-JUN-1991 (first entry)

DE Human Stem Cell Factor from HT1080 fibrosarcoma line.

KW Stem cell factor; SCF; leukopenia; AIDS; haematopoiesis.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25

FT Protein /label= sig_peptide

FT Protein /label= mat_protein

PN EP423980-A.

PD 24-APR-1991.

XX 04-OCT-1990; 90EP-0310899.

XX 01-OCT-1990; 90US-0589701.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

```

PR 24-AUG-1990; 90US-0573616.
PR 28-SEP-1990; 90WO-US05548.
XX
XX
PA (AMGE-) AMGEN INC.
XX
XX PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;
XX
XX DR MPI; 1991-119233/17.
XX
XX N-PSDB; AAQ11542.
XX
XX PT New naturally-occurring polypeptide stem cell factor analogues -
XX PT have haematopoietic biological activity of stem cell factor and
XX PT are used to treat eg leukaemia, AIDS, nerve damage and
XX PT infertility
XX
XX PS Disclosure; Fig 42; 127pp; English.
XX
XX CC The SCF has the ability to stimulate growth of primitive
XX CC progenitors including early hematopoietic progenitor cells and non-
XX CC hematopoietic stem cells such as neural stem cells and primordial
XX CC germ stem cells. The product may be used in a pharmaceutical
XX CC compsn. for treating, in a mammal, leukopenia, thrombocytopenia,
XX CC anaemia, AIDS, neoplasia, nerve damage, infertility and
XX CC intestinal damage.
XX CC See also AAR11708, AAQ11509-Q11543.
XX
XX SQ Sequence 273 AA;

Query_Match 97.1%; Score 1030; DB 12; Length 273;
Best Local Similarity 99.5%; Pred. No. 1.4e-100;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCYIQLLFPNPLVKTGICRRVTNNVDVTGLVANLPKDYMITLKYVPG 60
   |||||||
DB 1 MKKTQWILTCYIQLLFPNPLVKTGICRRVTNNVDVTGLVANLPKDYMITLKYVPG 60

QY 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120
   |||||||
DB 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120

QY 121 KDLKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASSETSDCVVSTLSPEKDSRVSVT 180
   |||||||
DB 121 KDLKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASSETSDCVVSTLSPEKDSRVSVT 180

QY 181 KPFMPLPVAASSLRNDSSSSNSK 203
   |||||||
DB 181 KPFMPLPVAASSLRNDSSSSNSK 203

RESULT 14
AAR20647
ID AAR20647 standard; Protein; 273 AA.
XX
XX AAR20647;
XX
AC AAR20647;
XX
DT 25-MAR-2003 (updated)
XX
DT 30-APR-1992 (first entry)
XX
DE Human mast cell growth factor.
XX
XX HMGF-2.4; hematopoietin; interleukin; IL-3; c-kit oncogene;
XX KM proliferation.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 1..25
XX FT /label= signal
XX FT 26..210
XX FT /label= extracellular
XX FT /note= "clained polypeptide"
XX FT 211..237
XX FT /label= transmembrane

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FT Region 238..273
FT FT /label= intracellular
XX
XX PN WO9200376-A.
XX
XX PD 09-JAN-1992.
XX
XX PF 14-JUN-1991; 91WO-US04274.
XX
XX PR 25-JUN-1990; 90US-0542264.
XX PR 10-AUG-1990; 90US-0565840.
XX PR 28-AUG-1990; 90US-0574152.
XX PR 21-SEP-1990; 90US-0586073.
XX PR 12-JUN-1991; 91US-0713715.
XX
XX PA (IMMV) IMMUNEX CORP.
XX
XX PI Williams DE, Lyman S;
XX
XX DR MPI; 1992-041558/05.
XX
XX DR N-PSDB; AAQ20845.
XX
XX CC New isolated DNA encoding human mast cell growth factor - useful in
XX CC stimulating proliferation of haematopoietic cells with growth factor,
XX CC to treat haemolytic and hypoproliferative anaemias
XX
XX PS Claim 10; Fig 4; 59pp; English.
XX
XX CC This human MGF has a mature extracellular region of 165 amino acids.
XX CC There is a second form of HMGF (see AAQ20844) resulting from an
XX CC alternative mRNA splicing event which deletes an exon encoding an
XX CC additional 28 amino acids beginning at amino acid 148 of the mature
XX CC protein. MGF is the ligand for the protein receptor expression product
XX CC of the c-kit proto-oncogene. MGF can be used to augment the
XX CC activity of other cytokines. It can influence early lymphoid or
XX CC myeloid development. See also AAQ20842-3 and AAQ22204-7.
XX
XX SQ Sequence 273 AA;

Query_Match 97.1%; Score 1030; DB 13; Length 273;
Best Local Similarity 99.5%; Pred. No. 1.4e-100;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCYIQLLFPNPLVKTGICRRVTNNVDVTGLVANLPKDYMITLKYVPG 60
   |||||||
DB 1 MKKTQWILTCYIQLLFPNPLVKTGICRRVTNNVDVTGLVANLPKDYMITLKYVPG 60

QY 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120
   |||||||
DB 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120

QY 121 KDLKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASSETSDCVVSTLSPEKDSRVSVT 180
   |||||||
DB 121 KDLKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASSETSDCVVSTLSPEKDSRVSVT 180

QY 181 KPFMPLPVAASSLRNDSSSSNSK 203
   |||||||
DB 181 KPFMPLPVAASSLRNDSSSSNSK 203

RESULT 15
AAR83978
ID AAR83978 standard; Protein; 273 AA.
XX
XX AAR83978;
XX
AC AAR83978;
XX
DT 25-MAR-2003 (updated)
XX
DT 15-MAY-1996 (first entry)
XX
DE Human stem cell factor derived from HT1080 fibrosarcoma cell line.
XX
XX Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;

```

KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KM transplant; neoplasia; myelosuppression; bone marrow; ss.
XX
OS Homo sapiens.

Key Location/Qualifiers
FH Peptide 1..25
FT /label= sig_peptide
FT 26..248
FT Protein /label= mat_SCF

EP676470-A1.

11-OCT-1995.

04-OCT-1990; 95EP-0105391.

01-OCT-1990; 90US-0589701.

16-OCT-1989; 89US-0422383.

11-JUN-1990; 90US-0537198.

24-AUG-1990; 90US-0573616.

28-SEP-1990; 90WC-US05548.

(AMGE-) AMGEN INC.

Bosselman RA, Martin FH, Suggs SV, Zsebo KM;

WPI: 1995-346090/45.

N-PSDB; AAT04890.

New stem cell factor polypeptide(s) - for stimulating the growth of
primitive progenitor cells, esp. for treating disorders involving
blood cells

Claim 9; Fig 42; 127bp; English.

AAR83978 is a human stem cell factor (SCF) derived from the HT1080
fibrosarcoma cell line. Non-naturally occurring SCF and C-terminally
truncated polypeptides, having amino acid sequences sufficiently
duplicative of naturally occurring SCF, stimulate growth of primitive
progenitors such as haematopoietic progenitor cells, neural stem
cells and primordial germ stem cells. The peptides can be used in a
composition for treating leucopenia, anaemia or thrombocytopenia,
for enhancing engraftment of bone marrow during transplantation or
for bone marrow recovery after chemotherapy or radiation-induced bone
marrow aplasia or myelosuppression. They can also be used for
treating neoplasia, nerve damage, infertility, intestinal damage or
myeloproliferative disorders. Antibodies may be raised against the
peptides for use in detection or neutralisation of SCF in serum. SCF
may be useful for the treatment of AIDS and severe combined
immunodeficiency (SCID) states alone or in combination with other
factors such as IL-7
(Updated on 25-MAR-2003 to correct PF field.)

Sequence 273 AA;

Query Match 97.1%; Score 1030; DB 16; Length 273;
Best Local Similarity 99.5%; Pred. No. 1.4e-100;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLQLLFNPLVKEGICRNRYTNVVKVTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYLQLLFNPLVKEGICRNRYTNVVKVTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISSEWVOLSLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120
DB 61 MDVLPSCWISSEWVOLSLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120
QY 121 KDLKSKFKSPEPRLFTPEEFRIENRSIDAFKDVAVASETSDCVSSSTLSPKDSRVSVT 180
DB 121 KDLKSKFKSPEPRLFTPEEFRIENRSIDAFKDVAVASETSDCVSSSTLSPKDSRVSVT 180
QY 181 KPFMLPPVAASSLRNDSSSSNRK 203

Db 181 KPFMLPPVAASSLRNDSSSSNRK 203

Search completed: February 5, 2004, 15:05:13
Job time : 30.7961 secs

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OM protein - protein search, using sw model

Run on: February 5, 2004, 15:03:24 ; Search time 10.8871 Seconds
(without alignments)
808.360 Million cell updates/sec

Title: US-09-224-683-46
Perfect score: 1061
Sequence: 1 MKKTQTWILTCIYLQLLFFN.....AASLRNDSSSKYIYLI 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1061	100.0	208	3	US-08-836-252A-6 Sequence 6, Appl1
2	1061	100.0	208	3	US-08-482-918-46 Sequence 46, Appl1
3	1061	100.0	208	3	US-09-224-681-46 Sequence 46, Appl1
4	1061	100.0	208	3	US-08-336-728A-46 Sequence 46, Appl1
5	1030	97.1	273	1	US-08-220-379B-2 Sequence 2, Appl1
6	1030	97.1	273	2	US-08-628-428-9 Sequence 9, Appl1
7	1030	97.1	273	3	US-08-482-918-48 Sequence 48, Appl1
8	1030	97.1	273	3	US-08-482-918-49 Sequence 49, Appl1
9	1030	97.1	273	3	US-08-482-918-61 Sequence 61, Appl1
10	1030	97.1	273	3	US-09-224-681-48 Sequence 48, Appl1
11	1030	97.1	273	3	US-09-224-681-49 Sequence 49, Appl1
12	1030	97.1	273	3	US-09-224-681-61 Sequence 61, Appl1
13	1030	97.1	273	3	US-08-336-728A-48 Sequence 48, Appl1
14	1030	97.1	273	3	US-08-336-728A-49 Sequence 49, Appl1
15	1030	97.1	273	3	US-08-336-728A-61 Sequence 61, Appl1
16	1026	96.7	273	3	US-08-482-918-50 Sequence 50, Appl1
17	1026	96.7	273	3	US-09-224-681-50 Sequence 50, Appl1
18	1026	96.7	273	3	US-08-336-728A-50 Sequence 50, Appl1
19	1001	94.3	273	3	US-08-336-728A-54 Sequence 54, Appl1
20	975	91.9	424	5	PCT-US95-03866-14 Sequence 14, Appl1
21	974	91.8	424	5	PCT-US95-03866-12 Sequence 12, Appl1
22	920	86.7	266	3	US-08-482-918-57 Sequence 57, Appl1
23	920	86.7	266	3	US-09-224-681-57 Sequence 57, Appl1
24	920	86.7	266	3	US-08-336-728A-57 Sequence 57, Appl1
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26	897.5	84.6	274	3	US-08-336-728A-52 Sequence 52, Appl1
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38	865	81.5	195	3	US-08-482-918-44 Sequence 44, Appl1
39	865	81.5	195	3	US-09-224-681-44 Sequence 44, Appl1
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42	862.5	81.3	274	3	US-08-336-728A-51 Sequence 51, Appl1
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44	861	81.1	273	3	US-09-224-681-42 Sequence 42, Appl1
45	861	81.1	273	3	US-08-336-728A-42 Sequence 42, Appl1

ALIGNMENTS

RESULT 1
US-08-836-252A-6
; Sequence 6, Application US/08836252A
; Patent No. 6177556
; GENERAL INFORMATION:
; APPLICANT: Sharkey, Andrew M.
; APPLICANT: Smith, Stephen K.
; APPLICANT: Delliwig, Kimberley A.
; TITLE OF INVENTION: HUMAN SCF, A SPLICED VARIANT THERMOF, ITS
; TITLE OR INVENTION: PHARMACEUTICAL USE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, N.W. SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,252A
; FILING DATE: 31-JULY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB95/02547
; FILING DATE: 31-OCT-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422293.2
; FILING DATE: 04-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9508618.7
; FILING DATE: 28-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBERT W. ESMOND
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623.0550000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-836-252A-6

Query Match 100.0%; Score 1061; DB 3; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.9e-101;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYVLLFNPLVKTGICRNVTVNNVKDVTKLVANLPKDYMITLKYVVG 60
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QY 61 MDVLPSCWISSENVVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIYDDLVCEKENS 120
DB 61 MDVLPSCWISSENVVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIYDDLVCEKENS 120
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DB 121 KDLKSKFSPEPRILFTPEEPFRIFNRSIDAFKDFVASETSDCVSSTLSPEKDSRVSVT 180
QY 181 KPFLPVAASLRNDSSSNKYIYLI 208
DB 181 KPFLPVAASLRNDSSSNKYIYLI 208

RESULT 2

US-08-482-918-46
; Sequence 46, Application US/08482918
; Patent No. 6207417

GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-46

Query Match 100.0%; Score 1061; DB 3; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.9e-101;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKKTQWILTCIYVLLFNPLVKTGICRNVTVNNVKDVTKLVANLPKDYMITLKYVVG 60

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DB 61 MDVLPSCWISSENVVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVINIYDDLVCEKENS 120
QY 121 KDLKSKFSPEPRILFTPEEPFRIFNRSIDAFKDFVASETSDCVSSTLSPEKDSRVSVT 180
DB 121 KDLKSKFSPEPRILFTPEEPFRIFNRSIDAFKDFVASETSDCVSSTLSPEKDSRVSVT 180
QY 181 KPFLPVAASLRNDSSSNKYIYLI 208
DB 181 KPFLPVAASLRNDSSSNKYIYLI 208

RESULT 3

US-09-224-681-46
; Sequence 46, Application US/09224681
; Patent No. 6207454

GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
TRANSFER WITH STEM CELL FACTOR (SCF) POLYPEPTIDE
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:

INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-224-681-46

Query Match 100.0%; Score 1061; DB 3; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.9e-101;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCIYQLLFPNPLVKTGICRNRVTNNVQDVTKLVAANLPKQYMITLTKYVG 60
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RESULT 4

US-08-336-728A-46
Sequence 46, Application US/08336728A
Patent No. 6207802

GENERAL INFORMATION:

APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois

COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.

REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-336-728A-46

Query Match 100.0%; Score 1061; DB 3; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.9e-101;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCIYQLLFPNPLVKTGICRNRVTNNVQDVTKLVAANLPKQYMITLTKYVG 60
DB 1 MKKTQWTLTCIYQLLFPNPLVKTGICRNRVTNNVQDVTKLVAANLPKQYMITLTKYVG 60
QY 61 MDVLPBHCWISSEWVQSDSLTDLDFKSNISEGLSNYSIIDKLVINIYVDLVECKENSS 120
DB 61 MDVLPBHCWISSEWVQSDSLTDLDFKSNISEGLSNYSIIDKLVINIYVDLVECKENSS 120
QY 121 KDLKSFSPSPRLFTPEEFRIENRSIDAFKDFVAVSETSDCVVSTLSPEKDSRVSVT 180
DB 121 KDLKSFSPSPRLFTPEEFRIENRSIDAFKDFVAVSETSDCVVSTLSPEKDSRVSVT 180
QY 181 KPFLPVAASSLRNDSSSSNSKYIYL 208
DB 181 KPFLPVAASSLRNDSSSSNSKYIYL 208

RESULT 5

US-08-220-379B-2
Sequence 2, Application US/08220379B
Patent No. 5525708

GENERAL INFORMATION:

APPLICANT: No. 5525708ka, Karl
APPLICANT: Lobell, Robert B
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: United States of America
ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,379B
FILING DATE: 28-MAR-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Cytomed/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

FEATURE:
NAME/KEY: cleavage site
LOCATION: 164..165
US-08-220-3798-2

Query Match 97.1%; Score 1030; DB 1; Length 273;
Best Local Similarity 99.5%; Pred. No. 4.4e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCIYQLLFPNPLVKTGICRNRVTNNVADVTKLVANLPKQYMITLKYPVG 60
DB 1 MKKTQWTLTCIYQLLFPNPLVKTGICRNRVTNNVADVTKLVANLPKQYMITLKYPVG 60
QY 61 MDVLPSCWISEMNVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIIVDDLVECVKENS 120
DB 61 MDVLPSCWISEMNVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIIVDDLVECVKENS 120
QY 121 KDLKSFSPSPRLFTPEEFRIENRSIDAFKDFVAVSETSDCVSSTLSPEKDSRVSVT 180
DB 121 KDLKSFSPSPRLFTPEEFRIENRSIDAFKDFVAVSETSDCVSSTLSPEKDSRVSVT 180
QY 181 KPFLPVAASLRNDSSSNRK 203
DB 181 KPFLPVAASLRNDSSSNRK 203

RESULT 6

US-08-628-428-9
Sequence 9, Application US/08628428
Patent No. 5885962

GENERAL INFORMATION:
APPLICANT: Lu, Hsiang
TITLE OF INVENTION: SCF ANALOG COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,428
FILING DATE: 05-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Knight, Matthew W
REGISTRATION NUMBER: 36,846
REFERENCE/DOCKET NUMBER: A-400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..273
OTHER INFORMATION: /note="NOTE: Mature full length
OTHER INFORMATION: 1-248 SCF protein begins at amino acid 26; amino acid 1-25
OTHER INFORMATION: include Met and leader sequences for membrane band form of hu
OTHER INFORMATION: recombinant SCF."
US-08-628-428-9

Query Match 97.1%; Score 1030; DB 2; Length 273;
Best Local Similarity 99.5%; Pred. No. 4.4e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCIYQLLFPNPLVKTGICRNRVTNNVADVTKLVANLPKQYMITLKYPVG 60
DB 1 MKKTQWTLTCIYQLLFPNPLVKTGICRNRVTNNVADVTKLVANLPKQYMITLKYPVG 60
QY 61 MDVLPSCWISEMNVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIIVDDLVECVKENS 120
DB 61 MDVLPSCWISEMNVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIIVDDLVECVKENS 120
QY 121 KDLKSFSPSPRLFTPEEFRIENRSIDAFKDFVAVSETSDCVSSTLSPEKDSRVSVT 180
DB 121 KDLKSFSPSPRLFTPEEFRIENRSIDAFKDFVAVSETSDCVSSTLSPEKDSRVSVT 180
QY 181 KPFLPVAASLRNDSSSNRK 203
DB 181 KPFLPVAASLRNDSSSNRK 203

RESULT 7

US-08-482-918-48
Sequence 48, Application US/08482918
Patent No. 6207417

GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-48

Query Match 97.1%; Score 1030; DB 3; Length 273;
Best Local Similarity 99.5%; Pred. No. 4.4e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCIYQLLFPNPLVKTGICRNRVTNNVADVTKLVANLPKQYMITLKYPVG 60
DB 1 MKKTQWTLTCIYQLLFPNPLVKTGICRNRVTNNVADVTKLVANLPKQYMITLKYPVG 60
QY 61 MDVLPSCWISEMNVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIIVDDLVECVKENS 120
DB 61 MDVLPSCWISEMNVQVSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIIVDDLVECVKENS 120

Oy	121	KDLKSKSPSEPLFPPEEPFRFNNSIDAFKD PVAASSTPCVYSSITLSEKDSRVSVT	180
Db	121	KDLKSKSPSEPLFPPEEPFRFNNSIDAFKD PVAASSTPCVYSSITLSEKDSRVSVT	180
Oy	181	KPFMLPVAASSLRNDSSSNRK	203
Db	181	KPFMLPVAASSLRNDSSSNRK	203

RESULT 8

US-08-482-918-49
Sequence 49, Application US/08482918
Patent No. 6207417

GENERAL INFORMATION:
APPLICANT: Zeebo, Krizztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Sugus, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-482-918-49

Query Match	97.1%	Score 1030	DB 3	Length 273
Beat Local Similarity	99.5%	Pred. No. 4,4e-98		
Matches	Conservative	0	Mismatches	1
			Indels	0
			Gaps	0
QY	1	MKQTWTILTCYIQLLFPNLPVKTGECIRNRVTNNVAVDTLVANLPKDYMITLKYPVG	60	
Db	1	MKQTWTILTCYIQLLFPNLPVKTGECIRNRVTNNVAVDTLVANLPKDYMITLKYPVG	60	
QY	61	MDVLPSCHWISPMVQVQSDSLTDLLDKFSNTSEG.SNYSIIDKLVNIYDDLVCECKENS	120	
Db	61	MDVLPSCHWISPMVQVQSDSLTDLLDKFSNTSEG.SNYSIIDKLVNIYDDLVCECKENS	120	
QY	121	KDLKTSFKSPBEDRLFTPEBFRRIFNRSIDAFKDFVVASETSQCVSSITLSPKQSRVSVT	180	
Db	121	KDLKTSFKSPBEDRLFTPEBFRRIFNRSIDAFKDFVVASETSQCVSSITLSPKQSRVSVT	180	
QY	181	KPFMLPPVAASLRNDSSSSNKK	203	
Db	181	KPFMLPPVAASLRNDSSSSNKK	203	

RESULT 9
US-08-482-918-61

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Query Match      97.1%; Score 1030; DB 3; Length 273;
Best Local Similarity 99.5%; Pred. No. 4.4e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1 MKKQTMILTCIYQLLLFNPVLTBEGICNRNVNNNKDYTKLVANLPKQYMITLKVYPG 60
Db      1 MKKQTMILTCIYQLLLFNPVLTBEGICNRNVNNNKDYTKLVANLPKQYMITLKVYPG 60

Oy      61 MDVLPSCWISSEWVQSDSLTDLDPFNSISGTSNYSIIDKLVNIVDLVECKENSS 120
Db      61 MDVLPSCWISSEWVQSDSLTDLDPFNSISGTSNYSIIDKLVNIVDLVECKENSS 120

Oy      121 KDLKSKSPKPEPRLFTPEEFPRILFNRSIDAFAKDVVAASETSDCVVSSSTLSEPKDSRVSVT 180
Db      121 KDLKSKSPKPEPRLFTPEEFPRILFNRSIDAFAKDVVAASETSDCVVSSSTLSEPKDSRVSVT 180

Oy      181 KPFMILPVAASLRLNDSSSSNSK 203
Db      181 KPFMILPVAASLRLNDSSSSNSRK 203

; RESULT 10
; US-09-224-681-48
; Sequence 48, Application US/09224681
; Patent No. 6207454
; GENERAL INFORMATION:
; APPLICANT: Zaebo, Kristina M.
; APPLICANT: Besselman, Robert A.
; APPLICANT: Suggs, Sidney V.

```

APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESSES:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-48

Query Match 97.1%; Score 1030; DB 3; Length 273;
Best Local Similarity 99.5%; Pred. No. 4,4e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPLVKTGICRNRYNNVKQVTKLVANLPKQWMLTKYVPG 60
DB 1 MKKTQWILTCIYQLLEFNPLVKTGICRNRYNNVKQVTKLVANLPKQWMLTKYVPG 60
QY 61 MDVLPSCWISSENVVQSLTDLDKFSNISSEGLSNYSIIDKLXNIVDLYECVENSS 120
DB 61 MDVLPSCWISSENVVQSLTDLDKFSNISSEGLSNYSIIDKLXNIVDLYECVENSS 120
QY 121 KDLKSFKSPERLFTPEEPFRINRSIDAFKDFVAVSETSDCVSVSTLSPKDSRVSVT 180
DB 121 KDLKSFKSPERLFTPEEPFRINRSIDAFKDFVAVSETSDCVSVSTLSPKDSRVSVT 180

DB 121 KDLKSFKSPERLFTPEEPFRINRSIDAFKDFVAVSETSDCVSVSTLSPKDSRVSVT 180
QY 181 KPFLPVAASLRNDSSSSNSK 203
DB 181 KPFLPVAASLRNDSSSSNSK 203

RESULT 11
US-09-224-681-49
Sequence 49, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESSES:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-224-681-49

Query Match 97.1%; Score 1030; DB 3; Length 273;
Best Local Similarity 99.5%; Pred. No. 4,4e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYIQLLFNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYIQLLFNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISSEWVQSLDSDLTDLPKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQSLDSDLTDLPKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120
QY 121 KDLKKSFKSPERLPTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKKSFKSPERLPTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFLPVAASSLRNDSSSSNRK 203
DB 181 KPFLPVAASSLRNDSSSSNRK 203

RESULT 12

US-09-224-681-61
Sequence 61, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383

FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 0101/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:

INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-224-681-61

Query Match 97.1%; Score 1030; DB 3; Length 273;
Best Local Similarity 99.5%; Pred. No. 4,4e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYIQLLFNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYIQLLFNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISSEWVQSLDSDLTDLPKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQSLDSDLTDLPKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120
QY 121 KDLKKSFKSPERLPTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKKSFKSPERLPTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFLPVAASSLRNDSSSSNRK 203
DB 181 KPFLPVAASSLRNDSSSSNRK 203

RESULT 13

US-08-336-728A-48
Sequence 48, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616

FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-48

Query Match 97.1%; Score 1030; DB 3; Length 273;
Best Local Similarity 99.5%; Pred. No. 4.4e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVQDTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVQDTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISBMVQVSDSLTDLDKFSNISEGLSNYSIIDKLVINIYDDVVECVKENS 120
DB 61 MDVLPSCWISBMVQVSDSLTDLDKFSNISEGLSNYSIIDKLVINIYDDVVECVKENS 120
QY 121 KDLKSFSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
DB 121 KDLKSFSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
QY 181 KPFMLPVAASLRNDSSSNRK 203
DB 181 KPFMLPVAASLRNDSSSNRK 203

RESULT 14
US-08-336-728A-49

Sequence 49, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Sugas, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255

FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-49

Query Match 97.1%; Score 1030; DB 3; Length 273;
Best Local Similarity 99.5%; Pred. No. 4.4e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVQDTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVQDTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISBMVQVSDSLTDLDKFSNISEGLSNYSIIDKLVINIYDDVVECVKENS 120
DB 61 MDVLPSCWISBMVQVSDSLTDLDKFSNISEGLSNYSIIDKLVINIYDDVVECVKENS 120
QY 121 KDLKSFSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
DB 121 KDLKSFSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
QY 181 KPFMLPVAASLRNDSSSNRK 203
DB 181 KPFMLPVAASLRNDSSSNRK 203

RESULT 15
US-08-336-728A-61

Sequence 61, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Sugas, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-61

Query Match 97.1%; Score 1030; DB 3; length 273;
Best Local Similarity 99.5%; Pred. No. 4,4e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVQDVTKLVAIIPKDYMITLKYVPG	60
DB	1	MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVQDVTKLVAIIPKDYMITLKYVPG	60
QY	61	MDVLPSCWTSSEWVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVINIVDDLVCEVKENSS	120
DB	61	MDVLPSCWTSSEWVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVINIVDDLVCEVKENSS	120
QY	121	KDLKSKSPSPPEPRLFTPEEPFRIIPRSIDAFKDFVASETSDCVSSTLSPEKDSRVSVT	180
DB	121	KDLKSKSPSPPEPRLFTPEEPFRIIPRSIDAFKDFVASETSDCVSSTLSPEKDSRVSVT	180
QY	181	KPFMLPVAASSLNDSSSSNSK	203
DB	181	KPFMLPVAASSLNDSSSSNSK	203

Search completed: February 5, 2004, 15:12:22
Job time : 10.8871 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 15:07:35 / Search time 23.2066 Seconds
(without alignments)
1876.686 Million cell updates/sec

Title: US-09-224-683-46

Perfect score: 1061
Sequence: 1 MKKTQTWILTCIYLQLLFN.....AASSLRNDSNSSKXYILI 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1061	100.0	208	9	US-09-005-243-46 Sequence 46, Appl
2	1061	100.0	208	9	US-09-224-683-46 Sequence 53, Appl
3	1030	97.1	273	9	US-09-005-243-48 Sequence 48, Appl
4	1030	97.1	273	9	US-09-005-243-49 Sequence 49, Appl
5	1030	97.1	273	9	US-09-005-243-61 Sequence 48, Appl
6	1030	97.1	273	9	US-09-224-683-48 Sequence 49, Appl
7	1030	97.1	273	9	US-09-224-683-49 Sequence 49, Appl
8	1030	97.1	273	9	US-09-224-683-61 Sequence 61, Appl
9	1026	96.7	273	9	US-09-005-243-50 Sequence 50, Appl
10	1026	96.7	273	9	US-09-224-683-50 Sequence 50, Appl
11	920	86.7	266	9	US-09-005-243-57 Sequence 57, Appl
12	920	86.7	266	9	US-09-224-683-57 Sequence 57, Appl
13	890	83.9	245	9	US-09-005-243-63 Sequence 63, Appl
14	890	83.9	245	9	US-09-224-683-63 Sequence 63, Appl
15	884	83.3	271	9	US-09-005-243-52 Sequence 52, Appl

16	884	83.3	271	9	US-09-224-683-52	Sequence 52, Appl
17	875	82.5	273	9	US-09-005-243-53	Sequence 53, Appl
18	875	82.5	273	9	US-09-224-683-53	Sequence 53, Appl
19	865	81.5	195	9	US-09-005-243-44	Sequence 44, Appl
20	865	81.5	195	9	US-09-224-683-44	Sequence 44, Appl
21	862.5	81.3	274	9	US-09-005-243-51	Sequence 51, Appl
22	862.5	81.3	274	9	US-09-224-683-51	Sequence 51, Appl
23	861	81.1	273	9	US-09-005-243-42	Sequence 42, Appl
24	861	81.1	273	9	US-09-224-683-42	Sequence 42, Appl
25	855	80.6	273	9	US-09-005-243-55	Sequence 55, Appl
26	855	80.6	273	9	US-09-224-683-55	Sequence 55, Appl
27	855	80.6	273	15	US-10-132-345-4	Sequence 4, Appl
28	854	80.5	273	9	US-09-005-243-54	Sequence 54, Appl
29	854	80.5	273	9	US-09-224-683-54	Sequence 54, Appl
30	843	79.5	166	9	US-09-748-592-2	Sequence 2, Appl
31	839	79.1	164	10	US-09-903-327A-10	Sequence 10, Appl
32	839	79.1	165	12	US-10-320-231A-25	Sequence 25, Appl
33	839	79.1	165	15	US-10-053-355A-2	Sequence 2, Appl
34	839	79.1	393	15	US-10-270-555-1	Sequence 1, Appl
35	837	78.9	613	10	US-09-903-327A-14	Sequence 14, Appl
36	826	77.9	196	9	US-09-005-243-40	Sequence 40, Appl
37	826	77.9	196	9	US-09-224-683-40	Sequence 40, Appl
38	794	74.8	270	15	US-10-132-345-2	Sequence 2, Appl
39	679	64.0	165	9	US-09-005-243-1	Sequence 1, Appl
40	679	64.0	165	9	US-09-224-683-1	Sequence 1, Appl
41	667	62.9	393	15	US-10-270-555-2	Sequence 2, Appl
42	542.5	51.1	282	9	US-09-005-243-56	Sequence 56, Appl
43	542.5	51.1	282	9	US-09-224-683-56	Sequence 56, Appl
44	346	32.6	82	9	US-09-005-243-59	Sequence 59, Appl
45	346	32.6	82	9	US-09-224-683-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-09-005-243-46
Sequence 46, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESSES:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-46

Query Match 100.0%; Score 1061; DB 9; Length 208;
Best Local Similarity 100.0%; Pred. No. 6.9e-96;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWIIITCIYLLQLLFNPLVKTEGICRRNVTNNVDVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWIIITCIYLLQLLFNPLVKTEGICRRNVTNNVDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEMVVQSLDLDLDFKFSNISSEGLSNYSIIDKLVINIVDDIVECKENSS 120
DB 61 MDVLPSCWISSEMVVQSLDLDLDFKFSNISSEGLSNYSIIDKLVINIVDDIVECKENSS 120
QY 121 KDLKSFSPERPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
DB 121 KDLKSFSPERPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
QY 181 KPFMLPPVAASSLRNDSSSSNSKYIYL 208
DB 181 KPFMLPPVAASSLRNDSSSSNSKYIYL 208

RESULT 2
US-09-224-683-46
Sequence 46, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-46

Query Match 100.0%; Score 1061; DB 9; Length 208;
Best Local Similarity 100.0%; Pred. No. 6.9e-96;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWIIITCIYLLQLLFNPLVKTEGICRRNVTNNVDVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWIIITCIYLLQLLFNPLVKTEGICRRNVTNNVDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEMVVQSLDLDLDFKFSNISSEGLSNYSIIDKLVINIVDDIVECKENSS 120
DB 61 MDVLPSCWISSEMVVQSLDLDLDFKFSNISSEGLSNYSIIDKLVINIVDDIVECKENSS 120
QY 121 KDLKSFSPERPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
DB 121 KDLKSFSPERPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
QY 181 KPFMLPPVAASSLRNDSSSSNSKYIYL 208
DB 181 KPFMLPPVAASSLRNDSSSSNSKYIYL 208

RESULT 3
US-09-005-243-48
Sequence 48, Application US/0905243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-48

Query Match 97.1%; Score 1030; DB 9; Length 273;
Best Local Similarity 99.5%; Pred. No. 1.1e-92;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLLFNPVLKTEGICRNRVTNNVKDVTGLVANI,PKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYLLFNPVLKTEGICRNRVTNNVKDVTGLVANI,PKDYMITLKYVPG 60
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DB 61 MDVLPBHCWISSEWVQLSDSLTDLKFSNISGLSNYSIIDLVNIYDDLVCEKENS 120
QY 121 KDLKSKFSPEPRLFTPEEFRIENRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKSKFSPEPRLFTPEEFRIENRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFLMPVVAASLRNDSSSSNSK 203
DB 181 KPFLMPVVAASLRNDSSSSNSK 203

RESULT 4
US-09-005-243-49
Sequence 49, Application US/09005243
Patent No. US20020018763A1

GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-49

Query Match 97.1%; Score 1030; DB 9; Length 273;
Best Local Similarity 99.5%; Pred. No. 1.1e-92;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLLFNPVLKTEGICRNRVTNNVKDVTGLVANI,PKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYLLFNPVLKTEGICRNRVTNNVKDVTGLVANI,PKDYMITLKYVPG 60
QY 61 MDVLPBHCWISSEWVQLSDSLTDLKFSNISGLSNYSIIDLVNIYDDLVCEKENS 120
DB 61 MDVLPBHCWISSEWVQLSDSLTDLKFSNISGLSNYSIIDLVNIYDDLVCEKENS 120
QY 121 KDLKSKFSPEPRLFTPEEFRIENRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKSKFSPEPRLFTPEEFRIENRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180

Db 121 KOLKSFSPKSPRLFTPEEPFRIFNRSIDAFKDFVAVSETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFLPVAASSLRNDSSSSNSK 203
Db 181 KPFLPVAASSLRNDSSSSNSK 203

RESULT 5

US-09-005-243-61
Sequence 61, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-61

Query Match 97.1%; Score 1030; DB 9; Length 273;
Best Local Similarity 99.5%; Pred. No. 1.1e-92;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTOTWILTCIYIOLLFNPVLKTEGICRNKRVNNVADTVLVANLPKDYMITLKYPVG 60
Db 1 MKKTOTWILTCIYIOLLFNPVLKTEGICRNKRVNNVADTVLVANLPKDYMITLKYPVG 60
QY 61 MDVLPSCWISPMVQLSDSLTDLIDKPSNISSEGISNTSIIDKLVNIYDDLVECYKENS 120
Db 61 MDVLPSCWISPMVQLSDSLTDLIDKPSNISSEGISNTSIIDKLVNIYDDLVECYKENS 120
QY 121 KOLKSFSPKSPRLFTPEEPFRIFNRSIDAFKDFVAVSETSDCVSSTLSPKDSRVSVT 180
Db 121 KOLKSFSPKSPRLFTPEEPFRIFNRSIDAFKDFVAVSETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFLPVAASSLRNDSSSSNSK 203
Db 181 KPFLPVAASSLRNDSSSSNSK 203

RESULT 6

US-09-224-683-48
Sequence 48, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-48

Query Match 97.1%; Score 1030; DB 9; Length 273;
Best Local Similarity 99.5%; Pred. No. 1.1e-92;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVDVTKLVANLPKDYMTLLKYVVG 60
DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVDVTKLVANLPKDYMTLLKYVVG 60
QY 61 MDVLPSCWISSEWVQLSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVECKENSS 120
DB 61 MDVLPSCWISSEWVQLSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVECKENSS 120
QY 121 KDLKSKFSKPEPRLFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKSKFSKPEPRLFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFLPVAASSLRNDSSSSNSK 203
DB 181 KPFLPVAASSLRNDSSSSNSK 203

RESULT 7

US-09-224-683-49

Sequence 49, Application US/09224683

Patent No. US20020031491A1

GENERAL INFORMATION:

APPLICANT: Zeebo, Kristina M.

APPLICANT: Bosselman, Robert A.

APPLICANT: Suggs, Sidney V.

APPLICANT: Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor: Composition Claims

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:

ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/224,683

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/005,893

FILING DATE: 12-JAN-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/449,653

FILING DATE: 24-MAY-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/982,255

FILING DATE: 25-NOV-1992

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/589,701

FILING DATE: 01-OCT-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448

QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVDVTKLVANLPKDYMTLLKYVVG 60
DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVDVTKLVANLPKDYMTLLKYVVG 60
QY 61 MDVLPSCWISSEWVQLSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVECKENSS 120
DB 61 MDVLPSCWISSEWVQLSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVECKENSS 120
QY 121 KDLKSKFSKPEPRLFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKSKFSKPEPRLFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFLPVAASSLRNDSSSSNSK 203
DB 181 KPFLPVAASSLRNDSSSSNSK 203

US-09-224-683-49

Query Match 97.1%; Score 1030; DB 9; Length 273;
Best Local Similarity 99.5%; Pred. No. 1.1e-92;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVDVTKLVANLPKDYMTLLKYVVG 60
DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVDVTKLVANLPKDYMTLLKYVVG 60
QY 61 MDVLPSCWISSEWVQLSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVECKENSS 120
DB 61 MDVLPSCWISSEWVQLSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVECKENSS 120
QY 121 KDLKSKFSKPEPRLFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKSKFSKPEPRLFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFLPVAASSLRNDSSSSNSK 203
DB 181 KPFLPVAASSLRNDSSSSNSK 203

RESULT 8

US-09-224-683-61

Sequence 61, Application US/09224683

Patent No. US20020031491A1

GENERAL INFORMATION:

APPLICANT: Zeebo, Kristina M.

APPLICANT: Bosselman, Robert A.

APPLICANT: Suggs, Sidney V.

APPLICANT: Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor: Composition Claims

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:

ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/224,683

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-61

Query Match 97.1%; Score 1030; DB 9; Length 273;

Best Local Similarity 99.5%; Pred. No. 1.1e-92;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLENFPLVKTGICRNRVTNNVDVTKLVANLPKDYMTITLKYPG 60
DB 1 MKKTQWTLTCTIYQLLENFPLVKTGICRNRVTNNVDVTKLVANLPKDYMTITLKYPG 60
QY 61 MDVLPSCWISSEWVQLSDSLTDLDDKFSNISSEGLSNYSIIDKLVINIYDDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQLSDSLTDLDDKFSNISSEGLSNYSIIDKLVINIYDDLVCEKENS 120
QY 121 KDLKSPKSPERPLFTPEEFRIFRNSIDAFKDFVAVASSTSDCVVSTLSPKDSRVSVT 180
DB 121 KDLKSPKSPERPLFTPEEFRIFRNSIDAFKDFVAVASSTSDCVVSTLSPKDSRVSVT 180
QY 181 KPFMLPVAASLRNDSSSSNSK 203
DB 181 KPFMLPVAASLRNDSSSSNSK 203

RESULT 9

US-09-005-243-50
Sequence 50, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-50

Query Match 96.7%; Score 1026; DB 9; Length 273;

Best Local Similarity 99.0%; Pred. No. 2.7e-92;
Matches 201; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLENFPLVKTGICRNRVTNNVDVTKLVANLPKDYMTITLKYPG 60
DB 1 MKKTQWTLTCTIYQLLENFPLVKTGICRNRVTNNVDVTKLVANLPKDYMTITLKYPG 60
QY 61 MDVLPSCWISSEWVQLSDSLTDLDDKFSNISSEGLSNYSIIDKLVINIYDDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQLSDSLTDLDDKFSNISSEGLSNYSIIDKLVINIYDDLVCEKENS 120
QY 121 KDLKSPKSPERPLFTPEEFRIFRNSIDAFKDFVAVASSTSDCVVSTLSPKDSRVSVT 180
DB 121 KDLKSPKSPERPLFTPEEFRIFRNSIDAFKDFVAVASSTSDCVVSTLSPKDSRVSVT 180
QY 181 KPFMLPVAASLRNDSSSSNSK 203
DB 181 KPFMLPVAASLRNDSSSSNSK 203

RESULT 10

US-09-224-683-50

Sequence 50, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Susselmann, Robert A.
APPLICANT: Susselmann, Robert A.
APPLICANT: Susselmann, Robert A.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-50

Query Match 96.7%; Score 1026; DB 9; Length 273;
Best local Similarity 99.0%; Pred. No. 2,7e-92;
Matches 201; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKTQVWILTCIYQLLEPLVKTGICNRVTNNVKDVTKLVANIPKDYMTTLKYPG 60
DB 1 MKTQVWILTCIYQLLEPLVKTGICNRVTNNVKDVTKLVANIPKDYMTTLKYPG 60

QY 61 MDVLPSCHEMSEWVQLSDLTLDLKFNSISEGLSNYSIIDKLVNIVDLVECVKENS 120
DB 61 MDVLPSCHEMSEWVQLSDLTLDLKFNSISEGLSNYSIIDKLVNIVDLVECVKENS 120
QY 121 KDLKSFSPSPRLFTPEEFRIENRSIDAKDPVVASETSDCVVSTLSPEKSRVSVT 180
DB 121 KDLKSFSPSPRLFTPEEFRIENRSIDAKDPVVASETSDCVVSTLSPEKSRVSVT 180
QY 181 KPFMLPVAASLRNDSSSSNSK 203
DB 181 KPFMLPVAASLRNDSSSSNSK 203

RESULT 11
US-09-005-243-57
Sequence 57, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Susselmann, Robert A.
APPLICANT: Susselmann, Robert A.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 266 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-005-243-57

Query Match 86.7%; Score 920; DB 9; Length 266;
Best Local Similarity 92.6%; Pred. No. 6.3e-82;
Matches 188; Conservative 7; Mismatches 4; Indels 4; Gaps 4;

QY 1 MKKTQWTLITCIYLQLLFNPVLTGEGICRNRVTNNVKDVTKLVANLPKDYMTTLKYVPG 60
DB 1 MKKTQWTLITCIYLQLLFNPVLTGEGICRNRVT-DVKDVTKLVANLPKDYMTTLKYVPG 58
QY 61 MDVLPSCWISSEWVQSLDITLDFKPSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
DB 59 MDVLPSCWISSEWVQSLDITLDFKPSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 117
QY 121 KDLKSKFSKPEPRLTPEEPFRIFNRSIDAFKDFVVASSETDCVSSSTLSEKDSRVSVT 180
DB 118 KNVKKS-KSPEPRLTPEEPFRIFNRSIDAFKDFVVASSETDCVSSSTLSEKDSRVSVT 176
QY 181 KPFMLPVAASSLRNDSSSSNSK 203
DB 177 KPFMLPVAASSLRNDSSSSNSK 199

RESULT 12

US-09-224-683-57
Sequence 57, Application US/09224683
Patent No. US20020031491A1

GENERAL INFORMATION:

APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383

FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 266 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-57

Query Match 86.7%; Score 920; DB 9; Length 266;
Best Local Similarity 92.6%; Pred. No. 6.3e-82;
Matches 188; Conservative 7; Mismatches 4; Indels 4; Gaps 4;

QY 1 MKKTQWTLITCIYLQLLFNPVLTGEGICRNRVTNNVKDVTKLVANLPKDYMTTLKYVPG 60
DB 1 MKKTQWTLITCIYLQLLFNPVLTGEGICRNRVT-DVKDVTKLVANLPKDYMTTLKYVPG 58
QY 61 MDVLPSCWISSEWVQSLDITLDFKPSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
DB 59 MDVLPSCWISSEWVQSLDITLDFKPSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 117
QY 121 KDLKSKFSKPEPRLTPEEPFRIFNRSIDAFKDFVVASSETDCVSSSTLSEKDSRVSVT 180
DB 118 KNVKKS-KSPEPRLTPEEPFRIFNRSIDAFKDFVVASSETDCVSSSTLSEKDSRVSVT 176
QY 181 KPFMLPVAASSLRNDSSSSNSK 203
DB 177 KPFMLPVAASSLRNDSSSSNSK 199

RESULT 13

US-09-005-243-63
Sequence 63, Application US/09005243
Patent No. US20020018763A1

GENERAL INFORMATION:

APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-63

Query Match 83.9%; Score 890; DB 9; Length 245;
Best Local Similarity 100.0%; Pred. No. 4.9e-79;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVLTGICRNVTNNVKDVTXVANIPLKDYMTLKYVPG 60
DB 1 MKKTQWILTCIYQLLEFNPVLTGICRNVTNNVKDVTXVANIPLKDYMTLKYVPG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDFKSNISEGLSNYSIIDKLVINIVDDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDFKSNISEGLSNYSIIDKLVINIVDDLVECVKENS 120
QY 121 KDLKSKFSPERPLFTPEEFRIFNRSIDAFKDFVAVASTSDCVSSTISPEK 173
DB 121 KDLKSKFSPERPLFTPEEFRIFNRSIDAFKDFVAVASTSDCVSSTISPEK 173

RESULT 14
US-09-224-683-63
Sequence 63, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristztina M.
APPLICANT: Bosseelman, Robert A.
APPLICANT: Sugan, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-63

Query Match 83.9%; Score 890; DB 9; Length 245;
Best Local Similarity 100.0%; Pred. No. 4.9e-79;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVLTGICRNVTNNVKDVTXVANIPLKDYMTLKYVPG 60
DB 1 MKKTQWILTCIYQLLEFNPVLTGICRNVTNNVKDVTXVANIPLKDYMTLKYVPG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDFKSNISEGLSNYSIIDKLVINIVDDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDFKSNISEGLSNYSIIDKLVINIVDDLVECVKENS 120
QY 121 KDLKSKFSPERPLFTPEEFRIFNRSIDAFKDFVAVASTSDCVSSTISPEK 173
DB 121 KDLKSKFSPERPLFTPEEFRIFNRSIDAFKDFVAVASTSDCVSSTISPEK 173

RESULT 15
US-09-005-243-52
Sequence 52, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristztina M.
APPLICANT: Bosseelman, Robert A.
APPLICANT: Sugan, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

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OM protein - protein search, using sw model

Run on: February 5, 2004, 15:00:43 ; Search time 11.7466 Seconds
(without alignments)
1702.889 Million cell updates/sec

Title: US-09-224-683-46

Perfect score: 1061
Sequence: 1 MKKTQWILTCIYLQLLFN.....AASLNDSSSSNSKYIYL 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1030	97.1	273	2 A35974	mast cell growth f
2	899.5	84.8	274	2 I46575	c-kit ligand - pig
3	890	83.9	245	2 B61190	mast cell growth f
4	886.5	83.6	274	2 S47571	stem cell factor,
5	885.5	83.5	202	2 S58313	stem cell factor p
6	862.5	81.3	274	2 I46929	stem cell factor -
7	857	80.8	201	2 B35974	stem cell factor p
8	855	80.6	273	2 S65801	mast cell growth f
9	715	67.4	245	2 A37934	mast cell growth f
10	576.5	54.3	124	2 S29052	stem cell factor -
11	570.5	53.8	287	2 S70366	stem cell factor 1
12	562.5	53.0	287	2 S70367	stem cell factor p
13	479.5	45.2	253	2 S70367	stem cell factor p
14	175.5	16.3	51	2 B35971	mast cell growth f
15	172.5	16.3	49	2 A35971	mast cell growth f
16	97.5	9.2	1449	2 T16086	hypothetical prote
17	97	9.1	1447	2 F82909	hypothetical prote
18	94	8.9	1293	2 T27886	hypothetical prote
19	94	8.9	1813	2 T19295	hypothetical prote
20	92.5	8.7	164	2 B69616	cell-division init
21	92.5	8.7	512	2 G86773	citrate (pro-3S)-1
22	92	8.7	935	2 S63261	SEC21 protein - ye
23	91	8.6	1107	2 S61667	probable membrane
24	90.5	8.5	616	2 A69136	ATP-dependent Clp
25	89	8.4	1734	2 A41101	phospho ester-bind
26	88.5	8.3	545	2 B44054	orf2 protein - Jun
27	88.5	8.3	941	2 H84855	phosphoenolpyruvat
28	88	8.3	335	2 S44922	K18 antigen - Bnta
29	88	8.3	465	2 H97165	flagellar hook-len

30	88	8.3	702	2 P97352	membrane-associate
31	88	8.3	1690	2 T31670	DNA-directed RNA p
32	87.5	8.2	204005	2 T04005	probable protein k
33	87.5	8.2	966	2 S26235	phosphoenolpyruvat
34	87	8.2	664	2 T16411	hypothetical prote
35	86.5	8.2	246	2 T19850	hypothetical prote
36	86.5	8.2	436	2 F86486	protein F28J9.3 (1
37	86.5	8.2	844	2 S61104	BRO1 protein - Yea
38	86.5	8.2	1271	2 T08607	hypothetical prote
39	86	8.1	246	1 A64579	molybdenum ABC tra
40	86	8.1	496	2 G86887	threonine synthase
41	86	8.1	660	2 T22794	hypothetical prote
42	86	8.1	1334	2 T19493	hypothetical prote
43	85.5	8.1	222	2 T29762	hypothetical prote
44	85.5	8.1	614	2 B66461	probable protein k
45	85.5	8.1	636	2 A45949	mezozoite surface

ALIGNMENTS

RESULT 1

A35974
mast cell growth factor precursor - human
N:Alternate names: kit ligand; stem cell factor
C:Species: Homo sapiens (man)
C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C/Accession: A35974; A61190
S:Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.I
s, J.C.; Patel, A.C.; Fisher, E.F.; Erjavec, H.O.; Herrera, C.J.; Wrych, J.; Sachdev, I
Cell 63, 203-211, 1990
A>Title: Primary structure and functional expression of rat and human stem cell factor 1
A:Reference number: A35974; MUID:91004219; PMID:2208279
A/Accession: A35974
A/Molecule type: mRNA
A:Residues: 1-273 <MAR>
A/Cross-references: GB:M59964; NID:G37933; PIDN:AAA85450.1; PID:G37934
R:Anderson, D.M.; Williams, D.E.; Tushinski, R.; Gimpel, S.; Eisenman, J.; Camizaro, J
Cell Growth Differ. 2, 373-378, 1991
A>Title: Alternative splicing of mRNAs encoding human mast cell growth factor and localiza
A:Reference number: A61190; MUID:92172791; PMID:1724381
A/Accession: A61190
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A:Residues: 1-273 <AND>
A/Genetics:
C/Genes: GDB:MGF
A/Cross-references: GDB:128026; OMIM:184745
A/Map position: 12q22-12q22
C/Superfamily: mouse mast cell growth factor
C/Keywords: alternative splicing; extracellular protein; glycoprotein; transmembrane pro
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-273/Product: mast cell growth factor #status predicted <MCS>
F:26-189/Product: (or 26-190) mast cell growth factor, soluble form #status predicted <
F:215-237/Domain: transmembrane #status predicted <TM>
F:90,97,118,145,195/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match

Best Local Similarity 97.1%; Score 1030; DB 2; Length 273;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MKKTQWILTCIYLQLLFNPLVKTGICRNVTNNVQVTLVNLPRQWITLLKYVPG	60
DB	1	MKKTQWILTCIYLQLLFNPLVKTGICRNVTNNVQVTLVNLPRQWITLLKYVPG	60
QY	61	MDVLPSCWISSEWVQSLTDLDFENISEGLSNYSIIDKLVTIVVDLVECVENSS	120
DB	61	MDVLPSCWISSEWVQSLTDLDFENISEGLSNYSIIDKLVTIVVDLVECVENSS	120
QY	121	KDLKSKFSPERPLFTPEEFPRIFNRSIDAFQDVASSTSCVAVSTLSPKDSRVYT	180
DB	121	KDLKSKFSPERPLFTPEEFPRIFNRSIDAFQDVASSTSCVAVSTLSPKDSRVYT	180

QY 181 KPFPMLPPVAASSLRNDSSSSNSK 203
 Db 181 KPFPMLPPVAASSLRNDSSSSNSK 203

RESULT 2

c-kit ligand - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jul-2000
 C:Accession: I46575
 R:Zhang, Z.; Anthony, R.V.
 Biol. Reprod. 50, 95-102, 1994
 A:Title: Porcine stem cell factor/c-kit ligand: its molecular cloning and localization
 A:Reference number: I46575, PMID:94146218, PMID:7508758
 A:Accession: I46575
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-274 <ZHA>
 A:Cross-references: GB:I46575; NID:g164420; PIDN:AAA53670.1; PID:g164421
 C:Superfamily: mouse mast cell growth factor

Query Match 84.8%; Score 899.5; DB 2; Length 274;
 Best Local Similarity 86.3%; Pred. No. 1.2e-64;
 Matches 176; Conservative 17; Mismatches 10; Indels 1; Gaps 1;

QY 1 MKKTQWTLTCTIYQLLFNPLVKTGICRNRVTNNVADVTKLVANLPKDYMITLKYPG 60
 Db 1 MKKTQWTLTCTIYQLLFNPLVKTGICRNRVTNNVADVTKLVANLPKDYMITLKYPG 60

QY 61 MDVLPSCWISSEWVQSLDSDLTDLDKFSNISSEGLSNYSIIDKLVNIYDDLVCECKENSS 120
 Db 61 MDVLPSCWISSEWVQSLDSDLTDLDKFSNISSEGLSNYSIIDKLVNIYDDLVCECKENSHSF 120

QY 121 KDLKSFSPPEPRLFTPEEPFRIFNRSIDAFKDF-VVASETSDCVSSTLSPKDSRSV 179
 Db 121 ENVKSSKSPPEPRLFTPEEPFRIFNRSIDAFKDFLEWVAPKTSCTLSSTLSPKDSRSV 180

QY 180 TKFPMLPPVAASSLRNDSSSSNSK 203
 Db 181 TKFPMLPPVAASSLRNDSSSSNSK 204

RESULT 3

B61190
 mast cell growth factor, short form precursor - human
 N:Alternate names: kit ligand, short form; stem cell factor, short form
 C:Species: Homo sapiens (man)
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
 C:Accession: B61190
 R:Anderson, D.M.; Williams, D.E.; Tushinski, R.; Gimpel, S.; Eisenman, J.; Cannizzaro, L.
 Cell Growth Differ. 2, 373-378, 1991
 A:Title: Alternative splicing of mRNAs encoding human mast cell growth factor and localiza
 A:Reference number: A61190, PMID:92172791, PMID:1724381
 A:Accession: B61190
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-245 <AND>
 C:Comment: Alternative splicing produces this short form in which a predicted cleavage s
 C:Genetics:
 A:Gene: GDB:MGF
 A:Cross-references: GDB:128026; OMIM:184745
 A:Map position: 12q22-12q22
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: alternative splicing; glycoprotein; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <Sig>
 F:187-209/Domain: transmembrane #status predicted <TMN>
 F:190,97,118,145/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 83.9%; Score 890; DB 2; Length 245;
 Best Local Similarity 100.0%; Pred. No. 5.8e-64;
 Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLFNPLVKTGICRNRVTNNVADVTKLVANLPKDYMITLKYPG 60
 Db 1 MKKTQWTLTCTIYQLLFNPLVKTGICRNRVTNNVADVTKLVANLPKDYMITLKYPG 60

QY 61 MDVLPSCWISSEWVQSLDSDLTDLDKFSNISSEGLSNYSIIDKLVNIYDDLVCECKENSS 120
 Db 61 MDVLPSCWISSEWVQSLDSDLTDLDKFSNISSEGLSNYSIIDKLVNIYDDLVCECKENSS 120

QY 121 KDLKSFSPPEPRLFTPEEPFRIFNRSIDAFKDFVAVASETSDCVSSTLSPK 173
 Db 121 KDLKSFSPPEPRLFTPEEPFRIFNRSIDAFKDFVAVASETSDCVSSTLSPK 173

RESULT 4

S47571
 stem cell factor, longer isoform - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
 C:Accession: S47571
 R:Zhou, J.H.; Hukono, H.; Ohnaka, M.; Kubota, T.; Sakurai, M.
 Biochim. Biophys. Acta 1223, 148-150, 1994
 A:Title: Cloning and characterization of cDNAs encoding two normal isoforms of bovine st
 A:Reference number: S47571; PMID:94339176; PMID:7520283
 A:Accession: S47571
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-274 <ZHO>
 A:Cross-references: EMBL:D28934; NID:G538520; PIDN:BA06061.1; PID:G538521
 C:Superfamily: mouse mast cell growth factor

Query Match 83.6%; Score 886.5; DB 2; Length 274;
 Best Local Similarity 85.3%; Pred. No. 1.3e-63;
 Matches 174; Conservative 16; Mismatches 13; Indels 1; Gaps 1;

QY 1 MKKTQWTLTCTIYQLLFNPLVKTGICRNRVTNNVADVTKLVANLPKDYMITLKYPG 60
 Db 1 MKKTQWTLTCTIYQLLFNPLVKTGICRNRVTNNVADVTKLVANLPKDYMITLKYPG 60

QY 61 MDVLPSCWISSEWVQSLDSDLTDLDKFSNISSEGLSNYSIIDKLVNIYDDLVCECKENSS 120
 Db 61 MDVLPSCWISSEWVQSLDSDLTDLDKFSNISSEGLSNYSIIDKLVNIYDDLVCECKENSHSF 120

QY 121 KDLKSFSPPEPRLFTPEEPFRIFNRSIDAFKDF-VVASETSDCVSSTLSPKDSRSV 179
 Db 121 ENVKSSKSPPEPRLFTPEEPFRIFNRSIDAFKDFLEWVAPKTSCTLSSTLSPKDSRSV 180

QY 180 TKFPMLPPVAASSLRNDSSSSNSK 203
 Db 181 TKFPMLPPVAASSLRNDSSSSNSK 204

RESULT 5

S58313
 stem cell factor precursor - sheep (fragment)
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000
 C:Accession: S58313
 R:McInnes, C.J.; Logan, M.; Falconer, V.M.; Rawlins, P.; Huntly, J.; Haig, D.
 submitted to the EMBL Data Library, August 1995
 A:Description: Molecular cloning and biological activity of ovine stem cell factor.
 A:Reference number: S58313
 A:Accession: S58313
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-202 <MCI>
 A:Cross-references: EMBL:Z50743; NID:G940807; PIDN:CAA90620.1; PID:G940808
 C:Superfamily: mouse mast cell growth factor

Query Match 83.5%; Score 885.5; DB 2; Length 202;
 Best Local Similarity 86.1%; Pred. No. 1e-63;
 Matches 174; Conservative 15; Mismatches 12; Indels 1; Gaps 1;

QY 1 MKKTQWTLTCTIYQLLFNPLVKTGICRNRVTNNVADVTKLVANLPKDYMITLKYPG 60

```

Db      1 MKKTQWITTCIYQLLFNPLVHTQGIICRNRYTDDVKQVTKLVANLPRDYMITLKYPVG 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      61 MDVLPSCWISSENVVQLSDSLDLDLKFNSISGKSNYSIIDKLVINIVDLVECKENSS 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 MDVLPSCWISSENVVQLSDSLDLDLKFNSISGKSNYSIIDKLVINIVDLVECKENSHF 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      121 KDLKSKFKSPERPLFTPEEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPEKDSRVSV 179
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 ENVKSKSKSPERQFPEKFFGIFNKSIDAFKDLVIASTMECEVISTSSPEKDSRVSV 180
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      180 TKPFMLPVAASSLRNDSSSSN 201
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 TKPFMLPVAASSLRNDSSSSN 202
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
stem cell factor - dog
C:Species: Canis lupus familiaris (dog)
C>Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 21-Jul-2000
C:Accession: I46929
R:Shull, R.M.; Suggs, S.V.; Langley, K.E.; Okino, K.H.; Jacobsen, F.W.; Martin, F.H.
Exp. Hematol. 20, 1118-1124, 1992
A:Title: Canine stem cell factor (C-kit ligand) supports the survival of hematopoietic
A:Reference number: I46929; MUID:93106145; PMID:1281786
A:Accession: I46929
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-274 <SHU>
C:Superfamily: mouse mast cell growth factor

Query Match      81.3%; Score 862.5; DB 2; Length 274;
Best Local Similarity 84.8%; Pred. No. 1.le-61;
Matches 133; Conservative 13; Mismatches 17; Indels 1; Gaps 1;

Qy      1 MKKTQWITTCIYQLLFNPLVHTQGIICRNRYTDDVKQVTKLVANLPRDYMITLKYPVG 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MKKTQWITTCIYQLLFNPLVHTQGIICRNRYTDDVKQVTKLVANLPRDYMITLKYPVG 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      61 MDVLPSCWISSENVVQLSDSLDLDLKFNSISGKSNYSIIDKLVINIVDLVECKENSS 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 MDVLPSCWISSENVVQLSDSLDLDLKFNSISGKSNYSIIDKLVINIVDLVECKENSHF 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      121 KDLKSKFKSPERPLFTPEEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPEKDSRVSV 179
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 ENVKSKSKSPERQFPEKFFGIFNKSIDAFKDLVIASTMECEVISTSSPEKDSRVSV 180
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      180 TKPFMLPVAASSLRNDSSSSN 203
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 TKPFMLPVAASSLRNDSSSSN 204
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
stem cell factor protein precursor - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C:Accession: B35974; A39805
R:Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.F.
s, J.C.; Patel, A.C.; Fisher, E.F.; Erjavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev, R.
Cell 63, 203-211, 1990
A:Title: Primary structure and functional expression of rat and human stem cell factor
A:Reference number: A35974; MUID:91004219; PMID:2208279
A:Accession: B35974
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-201 <MAR>
A:Cross-references: GB:M59966; NID:9206861; PIDN:AAA42117.1; PID:9554507
R:Lu, H.S.; Clogston, C.L.; Wypych, J.; Fausset, P.R.; Lauren, S.; Mendiaz, E.A.; Zsebo,
J. Biol. Chem. 266, 8102-8107, 1991
A:Title: Amino acid sequence and post-translational modification of stem cell factor iso

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A:Reference number: A39805; MUID:91217037; PMID:1708771
A:Accession: A39805
A:Status: preliminary
A:Molecule type: protein
A:Residues: 'E', 27-190 <LUA>
C:Superfamily: mouse mast cell growth factor

Query Match      80.8%; Score 857; DB 2; Length 201;
Best Local Similarity 82.6%; Pred. No. 2e-61;
Matches 166; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

Qy      1 MKKTQWITTCIYQLLFNPLVHTQGIICRNRYTDDVKQVTKLVANLPRDYMITLKYPVG 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MKKTQWITTCIYQLLFNPLVHTQGIICRNRYTDDVKQVTKLVANLPRDYMITLKYPVG 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      61 MDVLPSCWISSENVVQLSDSLDLDLKFNSISGKSNYSIIDKLVINIVDLVECKENSS 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 MDVLPSCWISSENVVQLSDSLDLDLKFNSISGKSNYSIIDKLVINIVDLVECKENSHF 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      121 KDLKSKFKSPERPLFTPEEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPEKDSRVSV 180
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 KVKSKSLKPERNTPEEFRIFNRSIDAFKDFVVASDSDCVLSTLGEPEKDSRVSV 180
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      181 KPFLMLPVAASSLRNDSSSSN 201
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 KPFLMLPVAASSLRNDSSSSN 201
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
stem cell growth factor - mouse
N:Alternate names: hematopoietic growth factor KL, ligand steel factor; stem cell factor
C:Species: Mus musculus (house mouse)
C>Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 01-Dec-2000
C:Accession: S65801; A43751; A35976; A35972; A35973; I46768
R:Bedell, M.A.; Copeland, N.G.; Jenkins, N.A.
Genetics 142, 927-934, 1996
A:Title: Multiple pathways for Steel regulation suggested by genomic and sequence analysis
A:Reference number: S65801; MUID:97002551; PMID:8848898
A:Accession: S65801
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-273 <BED>
A:Cross-references: EMBL:U44725; NID:91172215; PIDN:AA052447.1; PID:91172216
R:Huang, E.J.; Nocka, K.H.; Buck, J.; Besmer, P.
Mol. Biol. Cell 3, 349-362, 1992
A:Title: Differential expression and processing of two cell associated forms of the kit-
A:Reference number: A43751; MUID:92330001; PMID:1378327
A:Accession: A43751
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-214, 'V', 216-273 <HUA>
A:Cross-references: GB:S40364; NID:9251668; PIDN:AA622554.2; PID:95705957
A:Note: the authors translated the codon TTG for residue 215 as Trp
R:Huang, E.; Nocka, K.; Beier, D.R.; Chu, T.Y.; Buck, J.; Lahm, H.W.; Wellner, D.; Leder
Cell 63, 225-233, 1990
A:Title: The hematopoietic growth factor kit is encoded by the Sl locus and is the ligand
A:Reference number: A35976; MUID:91004221; PMID:1698557
A:Accession: A35976
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-206, 'S', 208-270 <HU2>
A:Cross-references: GB:M38511
R:Anderson, D.M.; Lyman, S.D.; Baird, A.; Wignall, J.M.; Eisenman, J.; Rauch, C.; March,
Cell 63, 235-243, 1990
A:Title: Molecular cloning of mast cell growth factor, a hematopoietin that is active in
A:Reference number: A35977; MUID:91004223; PMID:1698558
A:Accession: A35977
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-273 <AND>
A:Cross-references: GB:M57647; GB:M38436; NID:9199151; PIDN:AAA39538.1; PID:9199152
R:Copeland, N.G.; Gilbert, D.J.; Cho, B.C.; Donovan, P.J.; Jenkins, N.A.; Cosman, D.; An

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mast cell growth factor - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
 C:Accession: A35971
 R:Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I.
 Cell 63, 167-174, 1990
 A>Title: Identification of a ligand for the c-kit proto-oncogene.
 A:Reference number: A35971; PMID:91004215; PMID:1698553
 A:Accession: A35971
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-49 <MIL>
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: transmembrane protein

	Query Match	Score	Length
Best Local Similarity	73.5%	172.5	49
Matches	36; Conservative	4; Mismatches	6; Indels
			Gaps
QY	28	ICGNATNNVQVETLVANLPEDWITTLKYGCGMVLPSHCISSEMTVO	76
Db	3	ICGNPTVDNVKDIKTVALENDWITTLNLYVAGMDVLS--NY-DWIVQ	48

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Search completed: February 5, 2004, 15:08:20
Job time : 12.7466 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 14:42:38 / Search time 6.58953 Seconds

(without alignments)
1484.408 Million cell updates/sec

Title: US-09-224-683-46

Perfect score: 1061

Sequence: 1 MKKTQTWLTCTIYQLLLEN.....AASSLRNDSNSSSKYIYL 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1030	97.1	273	1 SCF_HUMAN	P21583 homo sapien
2	908.5	85.6	274	1 SCF_FELCA	P79169 felis silve
3	899.5	84.8	274	1 SCF_PIG	Q29030 sus scrofa
4	898.5	84.7	274	1 SCF_HORSE	Q95nd2 equus caball
5	889.5	83.8	267	1 SCF_SHEEP	P79368 ovis aries
6	886.5	83.6	274	1 SCF_BOVIN	Q28132 bos taurus
7	885.5	83.5	274	1 SCF_CAPI	Q95m19 capra hircu
8	862.5	81.3	274	1 SCF_CANFA	Q06220 canis famli
9	861	81.1	273	1 SCF_RAT	P21581 rattus norv
10	859.5	81.0	274	1 SCF_MUSVI	Q95n18 mus muscla vis
11	855	80.6	273	1 SCF_MOUSE	P20826 mus musculu
12	570.5	53.8	287	1 SCF_COTJA	Q90314 coturnix co
13	562.5	53.0	287	1 SCF_CHICK	Q09108 gallus gall
14	102	9.6	981	1 SCFA_RICFE	Q94337 rickettsia
15	94	8.9	1813	1 UN13_CABEL	P27155 caenorhabdi
16	92	8.7	935	1 COG_YEAST	P32074 saccharomyc
17	91.5	8.6	496	1 MURE_WIGBR	Q8d221 wigleswort
18	90.5	8.5	1742	1 MYSC_HUMAN	Q9nq44 homo sapien
19	89	8.4	989	1 PTP3_DICDI	P54637 dictyosteli
20	88.5	8.3	545	1 VNC5_JCDNV	Q90054 junonia coe
21	87.5	8.2	966	1 CAPP_MBSA	Q02735 medicago sa
22	87	8.2	664	1 2AA4_CABEL	Q09543 caenorhabdi
23	86.5	8.2	844	1 BRO1_YEAST	P48582 saccharomyc
24	85.5	8.1	623	1 SYR_SULTO	Q971x1 sulfolobus
25	84.5	8.0	466	1 DNAA_PROMI	P22817 proteus mir
26	84.5	8.0	964	1 CAPP_TOBAC	P27154 nicotiana t
27	84.5	8.0	998	1 SCAD_RICAK	Q94x99 rickettsia
28	83	7.8	998	1 UBPT_SCHPO	Q9p755 schizosacia
29	82.5	7.8	451	1 DNAA_PASMU	Q9c1d4 pasteurella
30	82.5	7.8	991	1 SCAD_RICAU	Q94164 ureaplasma
31	82	7.7	235	1 PYRH_UREPA	Q9p466 ureaplasma
32	82	7.7	1140	1 YM96_YEAST	Q04893 saccharomyc
33	82	7.7	1188	1 PPSA_METUA	Q57962 methanococc

34	82	7.7	1224	1 MSNS_YEAST	P52918 saccharomyc
35	81	7.6	196	1 KITH_ASFB7	P18555 african swi
36	81	7.6	388	1 VA25_METUA	Q58431 methanococc
37	81	7.6	490	1 CPCK_MACPA	P33262 macaca fasc
38	81	7.6	626	1 GIDA_BUCBP	P53485 buchnera fasc
39	80.5	7.6	373	1 B1OF_HELPJ	Q921n1 helicobacte
40	80.5	7.6	442	1 YB1_ECOLI	P32690 escherichia
41	80.5	7.6	755	1 P100_HSVJ	P52519 human herpe
42	80.5	7.6	1039	1 PDP2_ARATH	Q9m9w8 arabidopsis
43	80.5	7.6	2238	1 RPL2_BUNYW	P20470 bunyavirus
44	80.5	7.6	4563	1 APB_HUMAN	P04114 homo sapien
45	80	7.5	480	1 YB9Q_YEAST	P38348 saccharomyc

ALIGNMENTS

RESULT 1	ID	SCF_HUMAN	STANDARD	PRT	273 AA.
AC	P21583	Q16487	Q9UOK7		
DT	01-MAY-1991	(Rel. 18, Created)			
DT	01-MAY-1991	(Rel. 18, Last sequence update)			
DT	15-SEP-2003	(Rel. 42, Last annotation update)			
DE	Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).				
GN	KITLG OR MGF OR SCF.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RX	MEDLINE=91004219; PubMed=2208279;				
RA	Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,				
RA	Morris C.F., McNamee I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,				
RA	Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,				
RA	Fisher E.F., Erjavec H.O., Herrera C.J., Wypych J., Sachdev R.K.,				
RA	Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zeebo K.M.,				
RT	"Primary structure and functional expression of rat and human stem				
RT	cell factor DNAs."				
RL	Cell 63:203-211(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM 2).				
RX	MEDLINE=99160429; PubMed=10049787;				
RA	Blair H.C., Julian B.A., Cao X., Jordan S.E., Dong S.S.,				
RT	"Parathyroid hormone-regulated production of stem cell factor in human				
RT	osteoblasts and osteoblast-like cells."				
RL	Biochem. Biophys. Res. Commun. 255:778-784(1999).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RA	Han C., Peng X., Yuan J., Qiang B.;				
RT	Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE OF 167-248 FROM N.A. (ISOFORM 2).				
RX	MEDLINE=92360843; PubMed=1379846;				
RA	Toyota M., Hinoda Y., Itoh F., Tsujisaki M., Inai K., Yachi A.;				
RT	"Expression of two types of Kit ligand mRNAs in human tumor cells."				
RL	Int. J. Hematol. 55:301-304(1992).				
CC	-1- FUNCTION: Stimulates the proliferation of mast cells. Able to				
CC	augment the proliferation of both myeloid and lymphoid				
CC	hematopoietic progenitors in bone marrow culture. Mediates also				
CC	cell-cell adhesion. Acts synergistically with other cytokines,				
CC	probably interleukins.				
CC	-1- SUBUNIT: Homodimer, non-covalently linked (probable).				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).				
CC	Also exists as a secreted soluble form (isoform 1 only) (By				
CC	similarity).				
CC	-1- ALTERNATIVE PRODUCTS:				
CC	Event=Alternative splicing; Named isoforms=2;				
CC	Name=1; Synonyms=SCF248;				
CC	IsoId=P21583-1; Sequence=Displayed;				
CC	Name=2; Synonyms=SCF220;				

```

CC      IsoId=P21583-2; Sequence=VSP_006022;
CC      DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC      -1- PTM: A soluble form is produced by proteolytic processing of
CC      isoform 1 in the extracellular domain.
CC      -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC      -1- DATABASE: NAME=Atlas Genet. Cyrogenet. Oncol. Haematol.;
CC      WWW="http://www.infobiogen.fr/services/chromancer/Genes/MGFR142.htm".
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M59964; AA85450.1; -
DR      EMBL; AF119835; AAD2048.1; -
DR      EMBL; AF400436; AAK92485.1; -
DR      EMBL; AF400437; AAK92486.1; -
DR      EMBL; S42571; AAB2846.2; -
DR      PIR; A35974; A35974.
DR      PIR; B61190; B61190.
DR      Genew; HGNC:6343; KITLG.
DR      GO; GO:0005173; P:stem cell factor receptor binding activity; TAS.
DR      GO; GO:0008283; P:cell proliferation; TAS.
DR      GO; GO:0007165; P:signal transduction; TAS.
DR      InterPro; IPR003452; SCF.
DR      Pfam; PF02404; SCF; 1.
DR      Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
DR      Alternative splicing.
KW      CHAIN
FT      SIGNAL 1 25
FT      CHAIN 26 273
FT      DOMAIN 26 214
FT      TRANSMEM 215 237
FT      DOMAIN 238 273
FT      DISULFID 29 114
FT      DISULFID 68 163
FT      CARBOHYD 90 90
FT      CARBOHYD 97 97
FT      CARBOHYD 118 118
FT      CARBOHYD 145 145
FT      CARBOHYD 195 195
FT      VARSPLIC 174 202
FT      CONFLICT 55 55
FT      CONFLICT 128 128
FT      CONFLICT 134 134
SO      SEQUENCE 273 AA; 30898 MW; 19FD362CB59C6607 CRC64;

Query Match      97.1%; Score 1030; DB 1; Length 273;
Best Local Similarity 99.5%; Pred. No. 8.7e-73;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 2
SCF_FELCA
ID SCF_FELCA STANDARD; PRT; 274 AA.
AC P79169;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
DE cell growth factor) (MGF).
GN KITLG OR SCF.
OS Fells silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxId=9685;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=97069946; PubMed=8912926;
RA Dunham S.P., Onions D.E.;
RT "The cloning and sequencing of cDNAs encoding two isoforms of feline
RT stem cell factor.";
RL DNA Seq. 6:233-237(1996).
CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
CC augment the proliferation of both myeloid and lymphoid
CC hematopoietic progenitors in bone marrow culture. Mediates also
CC cell-cell adhesion. Acts synergistically with other cytokines,
CC probably interleukins (By similarity).
CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
CC Also exists as a secreted soluble form (isoform 1 only) (By
CC similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P79169-1; Sequence=Displayed.
CC Name=2;
CC IsoId=P79169-2; Sequence=VSP_006021;
CC -1- PTM: A soluble form is produced by proteolytic processing of
CC isoform 1 in the extracellular domain (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; D50833; BAA09445.1; -
DR      InterPro; IPR003452; SCF.
DR      Pfam; PF02404; SCF; 1.
DR      Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
DR      Alternative splicing.
KW      CHAIN
FT      SIGNAL 1 25
FT      CHAIN 26 274
FT      DOMAIN 26 215
FT      TRANSMEM 215 238
FT      DOMAIN 239 274
FT      DISULFID 29 114
FT      DISULFID 68 164
FT      CARBOHYD 90 90
FT      CARBOHYD 97 97
FT      CARBOHYD 145 145
FT      CARBOHYD 196 196
FT      VARSPLIC 175 203
FT      CONFLICT 175 203
SO      SEQUENCE 274 AA; 30987 MW; C5B78DB4791237BE CRC64;

Query Match      85.6%; Score 908.5; DB 1; Length 274;
Best Local Similarity 88.2%; Pred. No. 2.2e-63;
Matches 180; Conservative 13; Mismatches 10; Indels 1; Gaps 1;

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```

QY 1 MKKTQWIIITCIYLLQLLFNPLVTEGICRNVTNNKQVTKLVANLPKQWITTKYVPG 60
DB 1 MKKTQWIIITCIYLLQLLFNPLVTEGICRNVTNNKQVTKLVANLPKQWITTKYVPG 60
QY 61 MDVLPSCWISSEWVQSLVSLTDLDPKFSNISSEGLSNYSIIDKLXVIVDVLVECVHEHS 120
DB 61 MDVLPSCWISSEWVQSLVSLTDLDPKFSNISSEGLSNYSIIDKLXVIVDVLVECVHEHS 120
QY 121 KDLKSKFSKSPERPLTPPEEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPKDSRVSV 179
DB 121 ENVKSSKSPERPLTPPEEFRIFNRSIDAFKDFLEWVAVKTSVCVISTLSPKDSRVSV 180
QY 180 TKPFMLPVAASSLRNDSSSSNK 203
DB 181 TKPFMLPVAASSLRNDSSSSNK 204

RESULT 3
SCF_PIG STANDARD; PRT; 274 AA.
AC 029030;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Klt ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast
DE cell growth factor) (MGF).
GN KITLG OR MGF.
OS Sus acrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
ON NCBI_TaxID=9823;
RX SEQUENCE FROM N.A.
RC TISSUE=Uterus;
MEDLINE=94146218; PubMed=7508758;
RA Zhang Z., Anthony R.V.;
RA "Porine stem cell factor/C-kit ligand: its molecular cloning and
RA localization within the uterus.";
RL Biol. Reprod. 50:95-102(1994).
CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
CC augment the proliferation of both myeloid and lymphoid
CC hematopoietic progenitors in bone marrow culture. Mediates also
CC cell-cell adhesion. Acts synergistically with other cytokines,
CC probably interleukins (By similarity).
CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
CC secreted soluble form (By similarity).
CC -1- PTM: A soluble form is produced by proteolytic processing of
CC the extracellular domain (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L07786; AAA53670.1; -.
DR PIR; I46575; I46575.
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF.1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
KW SIGNAL.
FT CHAIN 1 25
FT DOMAIN 26 274
FT TRANSMEM 216 238
FT DOMAIN 239 274
FT DISULFID 29 114
FT CARBOHYD 90 90
FT CARBOHYD 97 97

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FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 274 AA; 3118 MW; FF3C871AD7BA6A6 CRC64;
Query Match 84.8%; Score 899.5; DB 1; Length 274;
Best Local Similarity 86.3%; Pred. No. 1,le-62;
Matches 176; Conservative 17; Mismatches 10; Indels 1;
QY 1 MKKTQWIIITCIYLLQLLFNPLVTEGICRNVTNNKQVTKLVANLPKQWITTKYVPG 60
DB 1 MKKTQWIIITCIYLLQLLFNPLVTEGICRNVTNNKQVTKLVANLPKQWITTKYVPG 60
QY 61 MDVLPSCWISSEWVQSLVSLTDLDPKFSNISSEGLSNYSIIDKLXVIVDVLVECVHEHS 120
DB 61 MDVLPSCWISSEWVQSLVSLTDLDPKFSNISSEGLSNYSIIDKLXVIVDVLVECVHEHS 120
QY 121 KDLKSKFSKSPERPLTPPEEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPKDSRVSV 179
DB 121 ENVKSSKSPERPLTPPEEFRIFNRSIDAFKDFLEWVAVKTSVCVISTLSPKDSRVSV 180
QY 180 TKPFMLPVAASSLRNDSSSSNK 203
DB 181 TKPFMLPVAASSLRNDSSSSNK 204

RESULT 4
SCF_HORSE STANDARD; PRT; 274 AA.
AC 095MD2; 062765; Q95MG7; Q95MG8; Q9N1Y5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Klt ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast
DE cell growth factor) (MGF).
GN KITLG OR MGF OR SCF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
ON NCBI_TaxID=9796;
RX SEQUENCE OF 4-264 FROM N.A.
RA Terry R.R., Mickelson J.R., Schmutz S., Cochran E.G., Bailey E.;
RA "Equus caballus mast cell growth factor (MGF)".
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 12-267 FROM N.A.
RC TISSUE=Skin;
RA Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.;
RA "An Equine sequence homologous to stem cell factor (KIT-ligand)".;
RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE OF 107-202 AND 227-274 FROM N.A.
RA Terry R.R., Bailey E.F., Cochran E.G.;
RA "Evaluation of MGF as the candidate gene for Appaloosa spotting".;
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 147-197 FROM N.A.
RA Caetano A.R., Shine Y.-L., Lyons L.A., Laughlin T.F., O'Brien S.J.,
RA Murray J.D., Bowling A.T.;
RA "A primary Human-Horse comparative gene map.";
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
CC augment the proliferation of both myeloid and lymphoid
CC hematopoietic progenitors in bone marrow culture. Mediates also
CC cell-cell adhesion. Acts synergistically with other cytokines,
CC probably interleukins (By similarity).
CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
CC secreted soluble form (By similarity).
CC -1- PTM: A soluble form is produced by proteolytic processing of
CC the extracellular domain (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----

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DR	EMBL; AF401625; AAK94474.1;	-
DR	EMBL; AF053498; AAC97076.1;	-
DR	EMBL; AF367704; AAK63249.1;	-
DR	EMBL; AF367706; AAK63250.1;	-
DR	EMBL; AF130770; AAF36716.1;	-
DR	InterPro; IPR003452; SCR.	
DR	Pfam; PF02404; SCR; 1.	
KW	Growth factor; Glycoprotein;	Transmembrane; Signal; Cell adhesion
FT	SIGNAL	POTENTIAL.
FT	CHAIN	1 25 KIT LIGAND.
FT	DOMAIN	26 214 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	216 238 POTENTIAL.
FT	DOMAIN	239 274 CYTOPLASMIC (POTENTIAL).
FT	DISULFID	228 114 BY SIMILARITY.
FT	DISULFID	68 164 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	90 90 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	97 97 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	196 196 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	207 207 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CONFLICT	15 15 O -> P (IN REF. 2).
FT	CONFLICT	241 MISSING (IN REF. 3).
EQ	SEQUENCE	274 AA; 31217 MW; 96CDD4G9059132F2 CRC64;

Query Match	84.7%;	Score 898.5;	DB 1;	Length 274;
Best Local Similarity	86.8%;	Pred. No. 1.3e-62;		
Matches 177;	Conservative 15;	Mismatches 11;	Indels 1;	Gaps 1

QY	1	MKKQOTWLTCTCYLDLLEFNPLVKKEGIRNRRTNNVAKOVTKLVANLPKDYMTLTKXVVG	60
Db	1	MKKQOTWLTCTCYLDLLEFNPLVKKEGICENRVTDDVQVTKLVANLPKDYKTLTKXVVG	60
QY	61	MDVLESHCMISEMVAQLSDSLTDLDDKFSNISBGLSNYSIIDKLVNIVDLVECEVENS	120
Db	61	MDVLESHCMISEMVAQLSLTDLLEKFSNISBGLSNYSIIDKLVKIYDVLVECEHSS	120
QY	121	KDLKKSFKSPERLTLTPBEFFRIENFNSIDAFQDF-VVASETSDCVVSTLSPKDSRVY	179
Db	121	ENVKSKYSQSEBRLTLTPBEFFRIENFNSIDAFQDLWMVSKTSECYVSTLSPKDSRVY	180
QY	180	TKPFMLPVAASLRLNDSSSSNSK 203	
Db	181	TKPFMLPVAASLRLNDSSSSNRK 204	

RESULT	5
SCF_SHEEP	
ID	SCF_SHEEP
AC	P79368: 028591;
DT	28-FEB-2003 (Rel. 41, Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF) (Fragment).
GN	KITLG OR SCF.
OS	Ovis aries (Sheep).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Artiodactyla; Caprinae; Ovis.
OX	NCBI_TaxID:99940;
PN	[1]
PP	SEQUENCE OF 8-267 FROM N.A.
RC	TISSUE=Ovarian Follicle;
RX	MEDLINE=56413880; Pubmed=8662240;
RA	Tisdall D.J.; Quirke L.D.; Galloway S.M.;

```

RT "Ovine stem cell factor gene is located within a syntenic group on
RL chromosome 3 conserved across mammalian species.";
RL Mamm. Genome 7:472-473(1996).
RN [2]
RP SEQUENCE OF 1-202 FROM N.A.
RA McInnes C.J., Logan M., Falconer V.M., Rawlins P., Huntly J., Haig D.;
RT "Molecular cloning and biological activity of ovine stem cell
RT factor.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: Stimulates the proliferation of mast cells. Able to
CC augment the proliferation of both myeloid and lymphoid
CC hematopoietic progenitors in bone marrow culture. Mediates also
CC cell-cell adhesion. Acts synergistically with other cytokines,
CC probably interleukins (By similarity).
CC -! SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -! SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
CC secreted soluble form (By similarity).
CC -! PTM: A soluble form is produced by proteolytic processing of
CC the extracellular domain (By similarity).
CC -! SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
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DR	EMBL; U89874; AAB49491.1; -								
DR	EMBL; Z50743; CAA90620.1; -								
DR	PIR; S58313; S58313.								
DR	InterPro; IPR003452; SCF.								
DR	Pfam; PF02404; SCF; 1.								
KW	Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.								
FT	SIGNAL	1	25						
FT	CHAIN								
FT	DOMAIN	26	>267						
FT	TRANSMEM	216	238						
FT	DOMAIN	239	>267						
FT	DISULFID	29	114						
FT	DISULFID	68	164						
FT	CARBOHYD	90	90						
FT	CARBOHYD	97	97						
FT	CARBOHYD	145	145						
FT	CARBOHYD	196	196						
FT	NON TER	267	267						
EQ	SEQUENCE	267 AA;	30148 MW;	9D9D59E4B9EC841 CRC64;					

Query Match	83.8%	Score 889.5;	DB 1;	Length 267;
Best Local Similarity	85.8%	Pred. No. 6.2e-62;		
Matches 175; Conservative	15;	Mismatches 13;	Indels 1;	Gaps 1;

[illegible]

RESULT 6	
SCF_BOVIN	
ID _SCF_BOVIN	STANDARD;
	PRT; 274 AA

AC Q28132; Q9TU74;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Maat
 cell growth factor) (MGF).
 GN KITLG OR SCF.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Spleen;
 RX MEDLINE=94339176; PubMed=7520283;
 RA Zhou J., Hikono H., Ohtaki M., Kubota T., Sakurai M.;
 RT "Cloning and characterization of cDNAs encoding two normal isoforms of
 RT bovine stem cell factor.";
 RL Biochim. Biophys. Acta 1223:148-150(1994).
 RL [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Fetal brain;
 RA Kudo T.;
 RT "Bovine counterpart of stem cell factor.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RP SEQUENCE OF 204-239 FROM N.A., AND VARIANT ASP-218.
 RC STRAIN=Belgian Blue;
 RX MEDLINE=99315331; PubMed=10384045;
 RA Seitz J.J., Schmutz S.M., Thue T.D., Buchanan F.C.;
 RT "A missense mutation in the bovine MGF gene is associated with the
 RT roan phenotype in Belgian Blue and Shorthorn cattle.";
 RL Mamm. Genome 10:710-712(1999).
 CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
 CC augment the proliferation of both myeloid and lymphoid
 CC hematopoietic progenitors in bone marrow culture. Mediates also
 CC cell-cell adhesion. Acts synergistically with other cytokines,
 CC probably interleukins (By similarity).
 CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
 CC Also exists as a secreted soluble form (isoform 1 only) (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q28132-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q28132-2; Sequence=VSP 006020;
 CC -1- PTM: A soluble form is produced by proteolytic processing of
 CC isoform 1 in the extracellular domain (By similarity).
 CC -1- POLYMORPHISM: The Roan locus is responsible for the coat
 CC coloration of Belgian Blue and Shorthorn cattle. The solid-colored
 CC and white animals are homozygotes, and the roan animals, with
 CC intermingled colored and white hairs, are heterozygous. The roan
 CC phenotype is due to the Asp-218 mutation.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC -----
 CC EMBL: D28934; BA06061.1; -
 CC EMBL: AB033716; BA094808.1; -
 CC EMBL: AF120154; AA055355.1; -
 CC PIR: S47571; S47571.
 CC InterPro: IPR003452; SCF.
 CC Pfam: PF02404; SCF, 1.
 CC Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;

KM Alternative splicing; Polymorphism.
 FT SIGNAL 1 25
 FT CHAIN 26 274
 FT DOMAIN 26 274
 FT TRANSMEM 216 238
 FT DOMAIN 239 274
 FT DISULFID 29 114
 FT DISULFID 68 164
 FT CARBOHYD 90 90
 FT CARBOHYD 145 145
 FT CARBOHYD 196 196
 FT VARSPLIC 175 203
 FT FT
 FT VARIANT 218 218
 FT SEQUENCE 274 AA, 31014 MW, 64128 CRC64;
 SQ
 Query Match 83.6%; Score 886.5; DB 1; Length 274;
 Best Local Similarity 85.3%; Pred. No. 1,le-61;
 Matches 174; Conservative 16; Mismatches 13; Indels 1; Gaps 1;
 QY 1 MKKTQWILTCYLLQLLFNPVLTGICRNRVTNNVADVTGLVANLPDQWITTKYVPG 60
 DB 1 MKKTQWILTCYLLQLLFNPVLTGICRNRVTNNVADVTGLVANLPDQWITTKYVPG 60
 QY 61 MDVLPBHCWISPMVQLSDSLTDLLDKPSNISSEGLSNYSIIDKLVNYVDLVCEVKENS 120
 DB 61 MDVLPBHCWISPMVQLSDSLTDLLDKPSNISSEGLSNYSIIDKLVNYVDLVCEVKENS 120
 QY 121 KDLKSKFSPERPLFTPEERFRIPNRSIDAFKDF-VVASETDCVSVSTLSPKOSRVSV 179
 DB 121 EHVKKSSKSPERPRGTPPEKFFGIFNKSIDAFKDLDELIVASKMECVISSTSPKOSRVSV 180
 QY 180 TRPMLPVAASLRLNDSSSSNSK 203
 DB 181 TRPMLPVAASLRLNDSSSSNSK 204
 Db
 RESULT 7
 SCF CAPHI STANDARD; PRT; 274 AA.
 ID SCF CAPHI
 AC Q95MI9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Maat
 cell growth factor) (MGF).
 GN KITLG OR SCF.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OC NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Shiba; TISSUE=Brain;
 RA Yanagisawa N., Tanaka S., Yamanouchi K., Tojo H., Tachi C.;
 RT "Identification of splicing isoforms of caprine stem cell factor
 RT (gSCF) transcripts and expression patterns of the two major isoforms,
 RT gSCF25 and gSCF741, in the brain and the skin of adult and fetal
 RT Shiba goats, Capra hircus.";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
 CC augment the proliferation of both myeloid and lymphoid
 CC hematopoietic progenitors in bone marrow culture. Mediates also
 CC cell-cell adhesion. Acts synergistically with other cytokines,
 CC probably interleukins (By similarity).
 CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
 CC secreted soluble form (By similarity).
 CC -1- PTM: A soluble form is produced by proteolytic processing of
 CC the extracellular domain (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.

CC -----
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CC EMBL: AB002152; BAB71753.1; -
CC InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF. 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
FT SIGNAL 1 25
FT CHAIN 26 274
FT DOMAIN 26 215
FT TRANSMEM 216 238
FT DOMAIN 239 274
FT DISULFID 29 114
FT DISULFID 68 164
FT CARBOHYD 90 90
FT CARBOHYD 97 97
FT CARBOHYD 145 145
FT CARBOHYD 196 196
SQ SEQUENCE 274 AA; 31052 MW; BBF669A509EF65D CRC64;

Query Match 83.5%; Score 885.5; DB 1; Length 274;
Best local similarity 85.3%; Pred. No. 1.3e-61;
Matches 174; Conservative 16; Mismatches 13; Indels 1; Gaps 1;

QY 1 MKKTQWTLITCIYQLLFNPLVKTGICGRNVTNNVQVTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWTLITCIYQLLFNPLVKTGICGRNVTNNVQVTKLVANLPKDYMITLKYVPG 60

QY 61 MDVLPBHCWISENVVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVCEVKENSS 120
DB 61 MDVLPBHCWISENVVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVCEVKENSS 120

QY 121 KDLKSFSPSPRLFTPEEPFRIFNRSIDAFKDF-VVASETSDCVSSTLSPDKSRVSV 179
DB 121 ENVKKSKSPSPRLFTPEEPFRIFNRSIDAFKDF-VVASETSDCVSSTLSPDKSRVSV 180

QY 180 TKPFMLPVAASSLRNDSSSSNSK 203
DB 181 TKPFMLPVAASSLRNDSSSSNSK 204

RESULT 8
ID SCF CANFA STANDARD; PRT; 274 AA.
AC 006220; O8SPM6;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Klt ligand precursor (C-klt ligand) (Stem cell factor) (SCF) (Mast
DE cell growth factor) (MGF).
GN KITLG OR MGF.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN (1) SEQUENCE FROM N.A.
RP TISSUE=T-cell;
RC MEDLINE=93106145; PubMed=1281786;
RA Shull R.M., Suggs S.V., Langley K.E., Okino K.H., Jacobsen F.W.,
RA "Canine stem cell factor (C-klt ligand) supports the survival of
RT hematopoietic progenitors in long-term canine marrow culture.";
RL Exp. Hematol. 20:1118-1124 (1992).
RN (2)
RC SEQUENCE OF 17-274 FROM N.A.
RP TISSUE=tail;

RA Schmutz S.M., Berrere T.G.;
RT "MGF sequencing in the dog aids in mapping to CFA15";
RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: Stimulates the proliferation of mast cells. Able to
CC augment the proliferation of both myeloid and lymphoid
CC hematopoietic progenitors in bone marrow culture. Mediates also
CC cell-cell adhesion. Acts synergistically with other cytokines,
CC probably interleukins.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
CC secreted soluble form.
CC -!- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC -!- PTM: A soluble form is produced by proteolytic processing of
CC the extracellular domain (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SCF FAMILY.

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CC EMBL: S53329; AAB24619.1; -
CC PIR: I46929; I46929.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF. 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
FT SIGNAL 1 25
FT CHAIN 26 274
FT DOMAIN 26 215
FT TRANSMEM 216 238
FT DOMAIN 239 274
FT DISULFID 29 114
FT DISULFID 68 164
FT CARBOHYD 90 90
FT CARBOHYD 97 97
FT CARBOHYD 145 145
FT CARBOHYD 196 196
SQ SEQUENCE 274 AA; 30869 MW; 4182B9AD00793B CRC64;

Query Match 81.3%; Score 862.5; DB 1; Length 274;
Best local similarity 84.8%; Pred. No. 7.8e-60;
Matches 173; Conservative 13; Mismatches 17; Indels 1; Gaps 1;

QY 1 MKKTQWTLITCIYQLLFNPLVKTGICGRNVTNNVQVTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWTLITCIYQLLFNPLVKTGICGRNVTNNVQVTKLVANLPKDYMITLKYVPG 60

QY 61 MDVLPBHCWISENVVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVCEVKENSS 120
DB 61 MDVLPBHCWISENVVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVCEVKENSS 120

QY 121 KDLKSFSPSPRLFTPEEPFRIFNRSIDAFKDF-VVASETSDCVSSTLSPDKSRVSV 179
DB 121 ENVKKSKSPSPRLFTPEEPFRIFNRSIDAFKDF-VVASETSDCVSSTLSPDKSRVSV 180

QY 180 TKPFMLPVAASSLRNDSSSSNSK 203
DB 181 TKPFMLPVAASSLRNDSSSSNSK 204

RESULT 9
ID SCF RAT STANDARD; PRT; 273 AA.
AC P21581; O9QWZ4; Q922E7;
DT 01-MAY-1991 (Rel. 18, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Klt ligand precursor (C-klt ligand) (Stem cell factor) (SCF) (Mast
DE cell growth factor) (MGF) (Hematopoietic growth factor KL).


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CC      Name=1;
CC      IsoId=Q95N18-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q95N18-2; Sequence=VSP_006024;
CC      -1- PTM: A soluble form is produced by proteolytic processing of
CC      isoform 1 in the extracellular domain (By similarity).
CC      -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AY013712; MAG37434.1; -
DR      EMBL; AF23757; AAK7336.1; -
DR      InterPro; IPR003452; SCF.
DR      Pfam; PF02404; SCF, 1.
KW      Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
KW      Alternative splicing
FT      STGMAL 1
FT      CHAIN 25
FT      DOMAIN 26 274
FT      TRANSMEM 26 215
FT      TRANSMEM 216 238
FT      DOMAIN 239 274
FT      DISULFID 29 114
FT      DISULFID 68 164
FT      CARBOHYD 90 90
FT      CARBOHYD 97 97
FT      CARBOHYD 145 145
FT      CARBOHYD 196 196
FT      VARSPLIC 175 203
FT      CONFLICT 65 65
FT      CONFLICT 171 171
FT      CONFLICT 268 274
SQ      SEQUENCE 274 AA; 31034 MW; 5AC1619014AB5E72 CRC64;
Query Match 81.0%; Score 859.5; DB 1; Length 274;
Best Local Similarity 83.3%; Pred. No. 1.3e-59;
Matches 170; Conservative 16; Mismatches 17; Indels 1; Gaps 1;
QY 1 MKKTQWILTCYLYQLLRLPLVKTGICGNRYTNVKNVYKLVANLPRQVMTLKYVPG 60
DB 1 MKKTQWILTCYLYQLLRLPLVKTGICGNRYTNVKNVYKLVANLPRQVMTLKYVPG 60
QY 61 MDVLPSCWISSEWVQLSDSLTDLDPKFSNISGLSNYSITDKLVNIYVDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQLSDSLTDLDPKFSNISGLSNYSITDKLVNIYVDLVECVKENS 120
QY 121 KDLKSKFSKPEPRLFTPEEFRIENRSIDAFKDF-VVASETSDCVVSTLSEPKDSRVSV 179
DB 121 KDLKSKFSKPEPRLFTPEEFRIENRSIDAFKDF-VVASETSDCVVSTLSEPKDSRVSV 179
QY 121 ENVKSKPKQDEPHHFAPEDFRIFNRSIDALKDLLETVAKTSBCTVLPSTLSEPKDSRVSV 180
DB 121 ENVKSKPKQDEPHHFAPEDFRIFNRSIDALKDLLETVAKTSBCTVLPSTLSEPKDSRVSV 180
QY 180 TRPFMLPVAASLRNDSSSNK 203
DB 180 TRPFMLPVAASLRNDSSSNK 203
DB 181 TRPFMLPVAASLRNDSSSNK 204
RESULT 11
SCF_MOUSE STANDARD; PRT; 273 AA.
AC P20826; P97332; Q62524; Q64222; Q921N5;
AC P20826; P97332; Q62524; Q64222; Q921N5;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE K1t ligand precursor (C-K1t ligand) (Stem cell factor) (SCF) (Mast
DE cell growth factor) (MGF) (Hematopoietic growth factor KL) (Steel
DE factor).
```

```
GN KITLG OR KITL OR MGF OR SL OR SLF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=MCB6F1;
RX MEDLINE=9100423; PubMed=1698558;
RA Anderson D.M., Lyman S.D., Baird A., Wignall J.M., Eisenman J.,
RA Rauch C., March C.J., Boswell H.S., Gimpe S.D., Cosman D.,
RA Williams D.E.;
RT "Molecular cloning of mast cell growth factor, a hematopoietin that
RT is active in both membrane bound and soluble forms."
RL Cell 63:235-243(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=92330001; PubMed=1378327;
RA Huang E.J., Nocka K.H., Buck J., Besmer P.;
RT "Differential expression and processing of two cell associated forms
RT of the kit-ligand: KL-1 and KL-2."
RL Mol. Biol. Cell 3:349-362(1992).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=MCB6F1;
RX MEDLINE=91160046; PubMed=1705866;
RA Flanagan J.G., Chan D.C., Leder P.;
RT "Transmembrane form of the kit ligand growth factor is determined by
RT alternative splicing and is missing in the Sld mutant."
RL Cell 64:1025-1035(1991).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=93012940; PubMed=1383087;
RA Brannan C.I., Bedell M.A., Resnick J.L., Eppig J.J., Handel M.A.,
RA Williams D.E., Lyman S.D., Donovan P.J., Jenkins N.A.,
RA Copeland N.G.;
RT "Developmental abnormalities in Steel17H mice result from a splicing
RT defect in the steel factor cytoplasmic tail."
RL Genes Dev. 6:1832-1842(1992).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J;
RX MEDLINE=97002551; PubMed=8849898;
RA Bedell M.A., Copeland N.G., Jenkins N.A.;
RT "Multiple pathways for Steel regulation suggested by genomic and
RT sequence analysis of the murine Steel gene."
RL Genetics 142:927-934(1996).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS PRO-193 AND SER-207.
RC STRAIN=C3H/HeJ; TISSUE=Brain;
RX MEDLINE=97032534; PubMed=8875893;
RA Graw J., Loester J., Neuhauser-Klaus A., Pretsch W.,
RA Schmitt-John T.;
RT "Molecular analysis of two new Steel mutations in mice shows a
RT transversion or an insertion."
RL Mamm. Genome 7:843-846(1996).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS SER-122; PRO-193 AND
RP SER-207.
RC STRAIN=102/E1 x C3H/HeJ;
RX MEDLINE=98025115; PubMed=9360640;
RA Graw J., Neuhauser-Klaus A., Pretsch W.;
RT "Detection of a point mutation (A to G) in exon 5 of the murine Mgf
RT gene defines a novel allele at the Steel locus with a weak
RT phenotype."
RL Mutat. Res. 382:75-78(1997).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakata I.,
```


RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasikawa T., Saito R.,
 RA Kadota K., Matsumoto H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi G., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikiado I., Posole G., Quackenbush J.,
 RA Schiraldi L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuta M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boftelli D., Bojunga N., Carninci P., de Bonaldi M.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbarts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Yashizaki Y.,
 RA "Functional annotation of a full-length mouse cDNA collection."
 RT Nature 409:685-690(2001).
 RL [19]
 RN SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT SER-207.
 RP MEDLINE=22388257; PubMed=12477932;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Sodegren E.J., Lu X., Gibbs R.A.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodegren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butcherfield Y.S.N., Krzyzanski M.I., Skalski D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [10]
 RN SEQUENCE OF 1-270 FROM N.A. (ISOFORM 1), AND SEQUENCE OF 26-65.
 RP MEDLINE=91004221; PubMed=1698557;
 RX Huang E., Nocka K., Belter D.R., Chu T.Y., Buck J., Lahm H.W.,
 RA Wellner D., Leder P., Besmer P.,
 RT "The hematopoietic growth factor KL is encoded by the Sl locus and is
 the ligand of the c-kit receptor, the gene product of the w locus.";
 RL Cell 63:225-233(1990).
 RN [11]
 RN SEQUENCE OF 1-201 FROM N.A.
 RP MEDLINE=91004220; PubMed=1698556;
 RX Zeebo K.M., Williams D.A., Geisler E.N., Broudy V.C., Martin F.H.,
 RA Atkins H.L., Hsu R.-Y., Birkett N.C., Okino K.H., Mardock D.C.,
 RA Jacobsen F.W., Langley K.E., Smith K.A., Takeishi T., Cattaneach B.M.,
 RA Gaili S.J., Stugs S.V.,
 RT "Stem cell factor is encoded at the Sl locus of the mouse and is the
 ligand for the c-kit tyrosine kinase receptor.";
 RL Cell 63:213-224(1990).
 RN [12]
 RN SEQUENCE OF 26-53.
 RP MEDLINE=91004216; PubMed=1698554;
 RX Copeland N.G., Gilbert D.J., Cho B.C., Donovan P.J., Jenkins N.A.,
 RA Cosman D., Anderson D., Lyman S.D., Williams D.E.,
 RT "Wast cell growth factor maps near the steel locus on mouse
 chromosome 10 and is deleted in a number of steel alleles.";
 RL Cell 63:175-183(1990).
 RN [13]
 RN PARTIAL SEQUENCE OF 26-78.
 RP MEDLINE=91004215; PubMed=1698553;
 RX Williams D.E., Eisenman J., Baild A., Rauch C., van Ness K.,
 RA March C.J., Park L.S., Martin U., Mochizuki D.Y., Boswell H.S.,
 RA Burgess G.S., Cosman D., Lyman S.D.,
 RT "Identification of a ligand for the c-kit proto-oncogene";

RL Cell 63:167-174(1990).
 CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
 CC augment the proliferation of both myeloid and lymphoid
 CC hematopoietic progenitors in bone marrow culture. Mediates also
 CC cell-cell adhesion. Acts synergistically with other cytokines,
 CC probably interleukins.
 CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
 CC Also exists as a secreted soluble form (isoform 1 only) (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=KL-1;
 CC IsoId=P20826-1; Sequence=Displayed;
 CC Name=2; Synonyms=KL-2;
 CC IsoId=P20826-2; Sequence=VSP 006023;
 CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -1- PTM: A soluble form is produced by proteolytic processing of
 CC isoform 1 in the extracellular domain.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC -----
 DR EMBL; M59915; AAA40095.1; -;
 DR EMBL; M57647; AAA39538.1; -;
 DR EMBL; S40534; AAA22555.2; -;
 DR EMBL; X68989; CAA48778.1; -;
 DR EMBL; U44724; -; NOT ANNOTATED_CDS.
 DR EMBL; U44725; AAC32447.1; -;
 DR EMBL; X93381; CAA64667.1; -;
 DR EMBL; X93382; CAA67698.1; -;
 DR EMBL; Y10287; CAA71329.1; -;
 DR EMBL; AK018777; BAB31402.1; -;
 DR EMBL; BC011322; AAH11322.1; -;
 DR EMBL; S40364; AAB22554.2; -;
 DR EMBL; M59912; AAA39539.1; -;
 DR PIR; A37934; A37934.
 DR PIR; S65801; S65801.
 DR MGI; MGI:96974; Kiti1.
 DR GO; GO:0016021; C:integral to membrane; IDA.
 Query Match 80.6%; Score 855; DB 1; Length 273;
 Best Local Similarity 82.3%; Pred. No. 2.9e-59;
 Matches 167; Conservative 16; Mismatches 20; Indels 0; Gaps 0;
 QY 1 MKKTQWITTCIYLDLLEFNPLVTEGICRNRVYNNVADVTGLVANNPKDWTITTKYVPG 60
 DB 1 MKKTQWITTCIYLDLLEFNPLVTEGICRNRVYNNVADVTGLVANNPKDWTITTKYVPG 60
 QY 61 MVLPSHCWISMVVQLDGLDLDKFSNISEGYSNIIDDKIYVNDLVECKENSS 120
 DB 61 MVLPSHCWISMVVQLDGLDLDKFSNISEGYSNIIDDKIYVNDLVECKENSS 120
 QY 121 KDLKSPKSPSPRLTPEEFRIFNRSIDAFKDFVAVASGTSVSTLSPKDSRVST 180
 DB 121 KDLKSPKSPSPRLTPEEFRIFNRSIDAFKDFVAVASGTSVSTLSPKDSRVST 180
 QY 181 KPPMLPVAASGLRNDSSSSNSK 203
 DB 181 KPPMLPVAASGLRNDSSSSNSK 203
 DT 28-FEB-2003 (Rel. 41, Created)

DT	28-PEB-2003 (Rel. 41, Last sequence update)
DT	28-PEB-2003 (Rel. 41, Last annotation update)
DE	Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
GN	KITLG OR SCF.
OS	Coturnix coturnix japonica (Japanese quail).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Coturnix.
OX	NCBI_TaxID=93934;
RA	[1]
RN	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX	MEDLINE=96283808; PubMed=8679698;
RT	Pedrite J.N., Kulik M.J.;
RL	"Cloning and characterization of cDNAs encoding two forms of avian stem cell factor.";
CC	Biochim. Biophys. Acta 1307:149-151(1996).
CC	- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).
CC	- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC	- CELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2). Also exists as a secreted soluble form (isoform 1 only) (By similarity).
CC	- ALTERNATIVE PRODUCTS:
CC	Event=Alternative splicing; Named isoforms=2;
CC	Name=1;
CC	IsoId=G090314-1; Sequence=Displayed;
CC	Name=2;
CC	IsoId=G090314-2; Sequence=VSP_006026;
CC	- PFM: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain.
CC	- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC	-----
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CC	-----
DR	EMBL; U43078; AAC59933.1; .
DR	EMBL; U43079; AAC59934.1; .
DR	InterPro; IPR003452; SCF.
DR	Pfam; PF02404; SCF; 1.
KW	Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion; Alternative splicing.
KM	SIGNAL
FT	1 25
FT	CHAIN
FT	DOMAIN
FT	TRANSMEM
FT	DOMAIN
FT	DISULFID
FT	DISULFID
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	VARSPLIC
SO	SEQUENCE
SO	287 AA; 32455 MW; ABAB1AEAA42A702E CRC64;
SO	Query Match 53.8%; Score 570.5; DB 1; Length 287;
SO	Best Local Similarity 55.1%; Pred.No.3.le-37;
SO	Matches 114; Conservative 37; Mismatches 51; Indels 5; Gaps 3;

```

Db      1 MKKAQTWITTFCCQALLINLVLKTOSSCGNPFVTDVNDIAKVLGNLPDVIYITLKYPK 60
Qy      61 MDVLPESHCMISEMWVQVSDSLTDLLDKF---SNISEGLSNYSIIDKLVNIYDVLVECYKE 117
Db      61 MDSPINHCMLHLMWVEFERSLHNLLQKQFVDISDMSDVLSNYSIINNLFRIINDLACIAF 120
Qy      118 NSSKD-LKSKRSKSPPEPLFTPEEFPRIINRSIDAKDQVVASSETSDCVVSTL-SPEKDS 175
Db      121 DKNQDFIKENHLYEEDRPIENEPFRLFNRTIEVYKEFADSLDKNDCTMPSTVETPENDS 180
Qy      176 RVSVTKPEMLPPVAASSLRNDSSSSNS 202
Db      181 RVAVTKTISFPVAASSLRNDSIGSNT 207

RESULT 13
SCF CHICK
ID SCF CHICK STANDARD; PRT; 287 AA.
AC 009108;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
cell growth factor) (MGF).
GN KITLG OR SCF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93273244; PubMed=7684722;
RA Zhou J., Ohtaki M., Sakurai M.;
RT "Sequence of a cDNA encoding chicken stem cell factor.";
RL Gene 127:269-270(1993).
CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
augment the proliferation of both myeloid and lymphoid
hematopoietic progenitors in bone marrow culture. Mediates also
cell-cell adhesion. Acts synergistically with other cytokines,
probably interleukins (By similarity).
CC -1- SUBUNIT: Homodimer; non-covalently linked (Probable).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
secreted soluble form (By similarity).
CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC -1- PTM: A soluble form is produced by proteolytic processing of
the extracellular domain (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D13516; BAA02733.1; -.
DR PIR; JN0637; JN0637.
DR InterPro; IPR0034552; SCF.
DR Pfam; PF02404; SCF; 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
CC CHAIN SIGNAL 1 25
FT CHAIN 26 287
FT DOMAIN 26 225
FT TRANSSEM 226 246
FT DOMAIN 247 287
FT DISULFID 29 117
FT DISULFID 68 167
FT CARBOHYD 100 100
FT CARBOHYD 149 149
FT CARBOHYD 200 200
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).

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SQ SEQUENCE 287 AA, 32328 MW, 6A89556ADCI52578 CRC64;
Query Match 53.0%; Score 562.5; DB 1; Length 287;
Best Local Similarity 54.6%; Pred. No. 1.3e-36;
Matches 113; Conservative 36; Mismatches 53; Indels 5; Gaps 3;

QY 1 MKKTQWILTCIYVLLFNPLVTEGICRNRYNNKVKLVANLPKDYMITLKYYVG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 MKKAQWITTCFCLQILLNPLVKAQSCGPNVTDVNDIAKLVGNLPNDYLITLKYPK 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 MVLPSHCWISSEWVQLSDSLDLKFNIS---SEGLSNYSIDKLVNIIVDVLCVKE 117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 MSLPNCWHLMLVPEPSSSLNHLQKFSDISMSDVLSNYSINNLTRIINDLWACIAF 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 118 NSSKD-LKSKFSPEPRLFTPEEPFRIPNRSIDAFVVAASEPSCVSTL-SPKXS 175
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 DKAKDIEKNGHLYEDRFIPENFRILFNSTIEVYKEFASLDKNDICMPTIVETPENDS 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 176 RVSVTKEPMLPPVAASLNDSSSSNS 202
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 RVAVTKTISFPVPAASLNDISGSNT 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
SCA4 RICEF STANDARD; PRT; 981 AA.
ID SCA4 RICEF STANDARD; PRT; 981 AA.
AC 09A37;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigenic heat-stable 120 kDa protein (PS120) (120 kDa antigen)
DE (Protein PS 120) (Fragment).
GN SCA4 OR D.
OS Rickettsia felis (Rickettsia azadi).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OC NCBI_Taxid=42862;
RN [1]
RP SEQUENCE FROM N.A.
RA Sekeyova Z., Roux V., Raoult D.
RT "Phylogenetic analysis of Rickettsia spp. by comparing the sequence of
RT gene D coding for an intracytoplasmic protein."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
-1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF196973; AAK31304.1; -.
CC Antigen.
FT NON_TER 1 1
FT NON_TER 981 981
SQ SEQUENCE 981 AA, 107514 MW, 7F18F421ECC262E1 CRC64;

Query Match 9.6%; Score 102; DB 1; Length 981;
Best Local Similarity 23.8%; Pred. No. 2.2;
Matches 62; Conservative 34; Mismatches 87; Indels 78; Gaps 14;

QY 19 FNPVLTGEGICRNRYNNKVD-----VTKLVANLPKDYMITLKYPGM-DV 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 628 FNTIAKTEAL--QNVTTKVLDSPIKAIKIGETLESITKVVAESPLNGODKADIVKMGGEA 685
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 64 LPSEH-----CWTSEWVQLSDSLDLK-----FSNISGLSNYSI----- 100
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 686 IASHKTMAPLEKSTLESVEKGAESITDLDDKMLTKGLVEGIYSGKANPEITSEKTYA 745
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 101 ----IDKLVNIIVD---LVLCVKE-----NSSDKLK-SFKSPPEPRLFTPEEPFRIF 144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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DB 746 VSRGIDKSTALPEDKQALKANAPALDRETONTLEGIKRONLGEPPER----DDIYNKA 801
QY 145 NRSIDAPDFV-----ASETSDCVSSSTLSPKX-SRVSYTK-----PFMLPP 187
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 802 QDVADALKNVTPVLDHAPKEKREVSSEEE-VYKKTSSILNDISKATIKANNFRAMLSPD 860
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 188 VAASSLRNDSSSSNSKYIYLI 208
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 861 GNLTLEKKAESTKVELV 881
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
ID UN13 CAEEL STANDARD; PRT; 1813 AA.
AC UN13 CAEEL STANDARD; PRT; 1813 AA.
DT 27715; 017665; Q23512; Q81095;
DT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Phorbol ester/diacylglycerol-binding protein unc-13 (Uncoordinated
DE protein 13).
DE UNC-13 OR ZK524.2.
GN Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodertinae; Caenorhabditis.
OC NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=Bristol N2.
RX MEDLINE=91288538; PubMed=2062851;
RA Maryama I.N., Brenner S.
RT "A phorbol ester/diacylglycerol-binding protein encoded by the unc-13
RT gene of Caenorhabditis elegans."
RT Proc. Natl. Acad. Sci. U.S.A. 88:5729-5733(1991).
RN [2]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
RC STRAIN=Bristol N2;
RX MEDLINE=20483775; PubMed=11029047;
RA Kohn R.E., Duert J.S., McManus J.R., Duke A., Rakow T.L., Maryama H.,
RA Moulder G., Maryama I.N., Barstead R.J., Rand J.B.
RT "Expression of multiple UNC-13 proteins in the Caenorhabditis elegans
RT nervous system."
RT Mol. Biol. Cell 11:3441-3452(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Gardner A.B., Lloyd C.R.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP REVISIONS, AND ALTERNATIVE SPLICING.
RA Durbin R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP ZINC AND PHORBOL-ESTERS BINDING.
RX MEDLINE=93075060; PubMed=1445255;
RA Ahmed S., Maryama I.N., Kozma R., Lee J., Brenner S., Lim L.;
RT "The Caenorhabditis elegans unc-13 gene product is a phospholipid-
RT dependent high-affinity phorbol ester receptor."
RL Biochem. J. 287:995-999(1992).
CC -1- FUNCTION: MAY FORM PART OF A SIGNAL TRANSDUCTION PATHWAY.
CC TRANSDUCING THE SIGNAL FROM DIACYLGLYCEROL TO EFFECTOR FUNCTIONS.
CC ONE SUCH FUNCTION COULD BE THE RELEASE OF NEUOTRANSMITTER FROM
CC NEURONS.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC Name=1; Synonyms=ZK524.2a;
CC IsoId=p27715-1; Sequence=Displayed;
CC Name=2;
CC IsoId=p27715-2; Sequence=VSP_004484;
CC Name=3;
CC IsoId=p27715-3; Sequence=VSP_004485;
CC Name=4; Synonyms=ZK524.2b;
CC IsoId=p27715-4; Sequence=VSP_004486, VSP_004487;
CC Note=No experimental confirmation available;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 14:59:08 / Search time 24.3526 Seconds
(without alignments)
2204.073 Million cell updates/sec

Title: US-09-224-683-46
Perfect score: 1061
Sequence: 1 MKKTQWILTCIYLQLLFFN.....AASLRNDSSSNKYIYLI 208

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

SPTREMBL_23: *
1: sp archaea: *
2: sp bacteria: *
3: sp fungi: *
4: sp human: *
5: sp invertebrate: *
6: sp mammal: *
7: sp mhc: *
8: sp organelle: *
9: sp phage: *
10: sp plant: *
11: sp rodent: *
12: sp virus: *
13: sp vertebrate: *
14: sp unclassified: *
15: sp virus: *
16: sp bacteriap: *
17: sp archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	855	80.6	208	11	Q64384
2	509	48.0	123	11	Q61854
3	480	45.2	160	11	Q6C9K1
4	327	30.8	271	13	Q9YGP2
5	273.5	25.8	270	13	Q8AYN7
6	116.5	11.0	1637	5	Q8ITM4
7	116.5	11.0	1711	5	Q8MWP2
8	116.5	11.0	1713	5	Q8MWP1
9	116.5	11.0	1716	5	Q8MWP2
10	100	9.4	3072	12	Q92645
11	97.5	9.2	1480	5	Q19545
12	97	9.1	1447	16	Q9PQJ8
13	96.5	9.1	1458	3	Q96VK6
14	96.5	9.1	1458	3	Q9P884
15	94.5	8.9	576	11	Q62970
16	94	8.9	906	5	Q8IEF0

17	94	8.9	1238	12	Q9EMP3	Q9emp3 amnacta moo
18	94	8.9	1816	5	Q81095	Q81095 caenorhabdi
19	93.5	8.8	579	11	Q99KM2	Q99KM2 mus musculu
20	93.5	8.8	722	11	Q8BZT8	Q8BZT8 mus musculu
21	92.5	8.7	164	16	P71021	P71021 bacillus su
22	92.5	8.7	512	16	Q9CGA7	Q9CGA7 lactococcus
23	92	8.7	188	5	Q9VRK2	Q9VRK2 dirosophila
24	92	8.7	2907	5	Q8IC71	Q8IC71 plasmodium
25	91.5	8.6	496	16	Q8D221	Q8D221 wiggleswort
26	91.5	8.6	976	2	Q54222	Q54222 staphylococ
27	91	8.6	317	5	Q9VTY2	Q9VTY2 dirosophila
28	91	8.6	317	5	Q8SX88	Q8SX88 dirosophila
29	91	8.6	422	12	Q911I4	Q911I4 white spot
30	91	8.6	1107	3	Q12271	Q12271 saccharomyc
31	90.5	8.5	254	11	Q9J1I6	Q9J1I6 rattus norv
32	90.5	8.5	616	17	Q26384	Q26384 methanobact
33	90	8.5	937	10	Q9MAL4	Q9MAL4 arabidopsis
34	90	8.5	967	5	Q8IKR7	Q8IKR7 plasmodium
35	90	8.5	1218	12	Q8VAV7	Q8VAV7 white spot
36	90	8.5	1219	12	Q911B1	Q911B1 white spot
37	90	8.5	1219	12	Q8QTD0	Q8QTD0 white spot
38	90	8.5	1501	3	Q86VL9	Q86VL9 botrytis ci
39	88.5	8.3	228	16	Q9XC73	Q9XC73 salmoneila
40	88.5	8.3	464	16	Q8EQ50	Q8EQ50 oceanobacil
41	88.5	8.3	941	10	Q9SINO	Q9SINO arabidopsis
42	88.5	8.3	963	10	Q8GVE9	Q8GVE9 arabidopsis
43	88.5	8.3	968	10	Q93XG8	Q93XG8 hydrilla ve
44	88.5	8.3	1056	16	Q8RE77	Q8RE77 fusobacteri
45	88.5	8.3	1570	5	Q9U0H8	Q9U0H8 plasmodium

ALIGNMENTS

RESULT 1

Q64384 PRELIMINARY; PRT; 208 AA.
ID Q64384
AC Q64384;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Mast cell growth factor (Fragment).
GN KITL OR MGF OR SL OR KL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92330001; PubMed=1378327;
RA Huang E.J., Nocka K.H., Buck J., Berner P.;
RT "Differential expression and processing of two cell associated forms
of the kit-ligand: KL-1 and KL-2".
RL Mol. Biol. Cell 3:349-362(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91160046; PubMed=1705866;
RA Flanagan J.G., Chan D.C., Leder P.;
RT "Transmembrane form of the kit ligand growth factor is determined by
alternative splicing and is missing in the slt mutant".
RL Cell 64:1025-1035(1991).
DR EMBL: 540536; AAA92556.2; -
DR EMBL: M64262; AAA9378.1; -
DR MGD; MGI:96974; Kitl.
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
FT NON TER 208
SQ SEQUENCE 208 AA; 23222 MW; C74DD63956EB817 CRC64;

Query Match 80.6%; Score 855; DB 11; Length 208;
Best Local Similarity 82.3%; Pred. No. 1.7e-61;
Matches 167; Conservative 16; Mismatches 20; Indels 0; Gaps 0;

Qy	1	MKKTQWMLFICCIYLOTLFFLPYAKTEGICIRNKNVTNNVDVRLVANI.PKQWMLTKCVPV	60
Qy	1	MKKTQWMLFICCIYLOTLFFLPYAKTEGICIRNKNVTNNVDVRLVANI.PKQWMLTKCVPV	60
Db	1	MKKTQWMLFICCIYLOTLFFLPYAKTEGICIRNKNVTNNVDVRLVANI.PKQWMLTKCVPV	60
Qy	61	MDVLP.SHCWISSENVVOLDSDLTDLDKFSNISEGHSNYSIDKLVNIYDDLVCEKENS	120
Qy	61	MDVLP.SHCWISSENVVOLDSDLTDLDKFSNISEGHSNYSIDKLVNIYDDLVCEKENS	120
Db	61	MDVLP.SHCWISSENVVOLDSDLTDLDKFSNISEGHSNYSIDKLVNIYDDLVCEKENS	120
Qy	121	KDLKKSFKSPEPLFTPEEPFERIENNSIDAFKDPVAVASSTDCVVSSTLSPEKDSRVSVT	180
Qy	121	KDLKKSFKSPEPLFTPEEPFERIENNSIDAFKDPVAVASSTDCVVSSTLSPEKDSRVSVT	180
Db	121	KDLKKSFKSPEPLFTPEEPFERIENNSIDAFKDPVAVASSTDCVVSSTLSPEKDSRVSVT	180
Qy	181	KPEMLP.VAASSLRNDSSSSNRK 203	
Qy	181	KPEMLP.VAASSLRNDSSSSNRK 203	
Db	181	KPEMLP.VAASSLRNDSSSSNRK 203	

RESULT 2			
061854			
ID	061854	PRELIMINARY;	PRT; 123 AA.
AC	Q61854;		
DT	01-NOV-1996 (TrEMBLrel. 01, Created)		
DT	01-NOV-1996 (TrEMBLrel. 01, last sequence update)		
DT	01-OCT-2002 (TrEMBLrel. 22, last annotation update)		
DE	Mast cell growth factor.		
GN	KITL OR MGF.		
OS	Mus musculus (Mouse).		
OC	Bakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain.		
RX	MEDLINE=97032534; PubMed=8875893;		
RL	Graw J., Loewer J., Neuhaeuser-Klaus A., Pretsch W., Schmitt-John T.,		
RT	transversion or an insertion."		
RL	Mamm. Genome 7:843-846(1996)."		
DR	EMBL; X95379; CA64666.1; "		
DR	MED; MGI:96974; Kiti1.		
DR	InterPro: IPR003452; SCF.		
DR	Pfam: PF02404; SCF.1		
SO	SEQUENCE	123 AA; 13892 MW; A872B4554B5D642 CRC64;	

	Query Match	48.0%;	Score 509;	DB 11;	Length 123;
	Best Local Similarity	81.0%;	Pred. No. 8.3e-34;		
	Matches	98; Conservative	10; Mismatches	13; Indels	0; Gaps
Oy	1 MKKTQWMLTLCYLOLLFNPLVKTGICRNKVTNNVDYTKLVANLPKDYMTLTKYVP	60			
Dd	1 MKKTQWMLTLCYLOLLFNPLVKTKEICGNPTVNVDITKLVANLPNDMYMTLTNTAVG	60			
Oy	61 MDVLPSHCWISBEMWVQLSDSLFDLDLPFNSISEGSNYIIDDKLVNIWDVLVECVKENSS	120			
Dd	61 MDVLPSHCWLRDWNVIQLSLSTLTLDKFSNISSEGLSNYSIIDDKLGKIVDDLVCMEBNAP	120			
Oy	121 K 121				
Dd	121 K 121				

RESULT 3

ID	QC8C9KI	PRELIMINARY;	PRT;	160 AA.
AC	QC8C9KI;			
DT	01-MAR-2003 (TEMBRprel. 23, Created)			
DT	01-MAR-2003 (TEMBRprel. 23, Last sequence update)			
DT	01-MAR-2003 (TEMBRprel. 23, Last annotation update)			
DS	Kit ligand (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI	TaxID=10090;			

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J; TISSUE=Thymus;
 RX MEDLINE=22354683; PubMed=12468651;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK041961; BAC31113.1; -.
 FT NON_TSR 160 160
 SQ SEQUENCE 160 AA; 17492 MF; B12AC581346AA6D CRC64;

Query Match	Similarity	Score	DB	Length
Best Local	80.7%	Pred. No. 2.5e-31		
Matches	92	Mismatches	10	Indels
			12	Gaps
			0	0

RESULT 4			
ID	Q9YGP2	PRELIMINARY;	PRT; 271 AA.
AC	Q9YGP2;		
DT	01-MAY-1999 (TREMBLrel. 10, Created)		
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	Steel factor.		
OS	Ambystoma mexicanum (Axolotl).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Caudata; Salamandroides; Ambystomidae;		
OC	Ambystoma.		
OX	NCBI_TaxID=8296;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=9929573; PubMed=10370116;		
RA	Parichy D.M., Stigson M., Voss S.R.;		
RT	"Genetic analysis of steel and the pc-M/versican-encoding gene Axpg as		
RT	candidates for the white (d) pigmentation mutant in the salamander		
RT	Ambystoma mexicanum."		
RL	Dev. Genes Evol. 209:349-356(1999).		
DR	EMBL; AF119044; AAD17253.1; --		
DR	InterPro; IPR003452; SCF.		
DR	Pfam; PF02404; SCF.1.		
QO	SEQUENCE 271 AA; 30075 MW; 876977ABF7D53EB4 CRC64;		

	Query Match	30.8% Best Local Similarity	Score 327; 39.2% Pred. No. 1,1e-19;	DB 13; Matches 83;	Mismatches 29;	Indels 22;	Gaps 6	Length 271;
Qy	1	MKKTQVMIILTCIYIQLLLF----	NPLVKTGECIGRRVYTNVVKDYTKLVANLPRKDMITLK	56				
Db	1	MKKTQVMIILTCIYIQLLLF----	CGNPVTADVNDIEKLVGNIPSPDYSISLE	53				
Qy	57	YVPEMDVLPRSHCMISEMWVQLSDSLTLLDLKESNISSELSVYSIITDKLVNIYVDDIVECVK	116					
Db	54	YVPMPSLPLQPCQWYLVHVKVSNLSLESIHKFPANTSQ--	NYSIMSNTLTALHGRNCLA	110				
Qy	117	-----ENSSKDLKSKFKSPERPLFLPPEEFRIENISDAFKDPVVAASETSDCVS--STLSP	171					
Db	111	SQILDNEEFITDPFFYDGE---FVPKEKFKVYVTITILLFKAIHMDDDSDTSELPTTBTP	167					
Qy	172	EKDSRVSYTKPEFMLPRVAASLRNDSSSSNKK	203					
Db	168	LSDLPLPGVATKPSAKESFMPSSSRKKRREGIPIANAK	199					

Best Local Similarity 23.0%; Pred. No. 0.93;
Matches 35; Conservative 41; Mismatches 57; Indels 19; Gaps 6;

QY 31 NRYTNVNVKVTKLVAN-----LPKDYMTLTKVPGM-DVLSHCWISGMVY---Q 76
Db 1223 HKINNNLKOITHIVINDNNTLOEQNRITYELQNKIKQIKVSVFTHTNINYSQOILINYSQ 1282
QY 77 LSDSLTDLDDKFSNISSEGLSN--YSIIDKLVINVD--DLVECVKENSXKDLKSKSPSP 132
Db 1283 AQNSPFNIFPMKFNINNDINSKRYNVOKKTETELINSYDIIN-YKNKNIDYIQQFNIIQ 1341
QY 133 RLFTPEEFRIFRNSIDAFKDFVASETSDCV 164
Db 1342 QLTNTTQNLHNIKONINHFKEYESHQTSIV 1373

RESULT 9

Q8MMH2 PRELIMINARY; PRT; 1716 AA.
AC Q8MMH2;
DT C1-OCT-2002 (T-EMBLrel. 22, Created)
DT C1-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT C1-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Reticulocyte binding protein homolog 4.
GN RH4.
OS Plasmodium falciparum (isolate NF54).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5843;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22030722; PubMed=12034462;
RA Kaneo O., Mu J.-B., Tsuboi T., Su X.-Z., Torii M.;
RT "Gene structure and expression of a Plasmodium falciparum 220-kDa
RT protein homologous to the Plasmodium vivax reticulocyte binding
RT protein."
RL Mol. Biochem. Parasitol. 121:275-278 (2002).
DR EMBL; AF432854; AAM47192.1;
SQ SEQUENCE 1716 AA; 205846 MW; 2A3DAC35B6FE226 CRC64;

Query Match 11.0%; Score 116.5; DB 5; Length 1716;
Best Local Similarity 23.0%; Pred. No. 0.93;
Matches 35; Conservative 41; Mismatches 57; Indels 19; Gaps 6;

QY 31 NRYTNVNVKVTKLVAN-----LPKDYMTLTKVPGM-DVLSHCWISGMVY---Q 76
Db 1220 HKINNNLKOITHIVINDNNTLOEQNRITYELQNKIKQIKVSVFTHTNINYSQOILINYSQ 1279
QY 77 LSDSLTDLDDKFSNISSEGLSN--YSIIDKLVINVD--DLVECVKENSXKDLKSKSPSP 132
Db 1280 AQNSPFNIFPMKFNINNDINSKRYNVOKKTETELINSYDIIN-YKNKNIDYIQQFNIIQ 1338
QY 133 RLFTPEEFRIFRNSIDAFKDFVASETSDCV 164
Db 1339 QLTNTTQNLHNIKONINHFKEYESHQTSIV 1370

RESULT 10

O92645 PRELIMINARY; PRT; 3072 AA.
AC O92645;
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Polyprotein.
OS clover yellow vein virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Polyviridae;
OC Potyvirus.
OX NCBI_TaxID=12198;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=No.30;
RA Uyeda I., Takahashi Y.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=No.30;

RX MEDLINE=97456254; PubMed=9311568;
RA Takahashi Y., Takahashi T., Uyeda I.;
RT "A cDNA clone to clover yellow vein potyvirus genome is highly
RT infectious."
RL Virus Genes 14:235-243 (1997).
CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
DR EMBL; AB011819; BA25147.1; -.

DR MEROPS; C04.008; -.
DR MEROPS; C06.001; -.
DR Interpro; IPR001410; DEAD.
DR Interpro; IPR001650; Helicase_C.
DR Interpro; IPR001730; Helicase_C4.
DR Interpro; IPR001456; Peptidase_C6.
DR Interpro; IPR001592; Polypeptide.
DR Interpro; IPR002540; Polypeptide.
DR Interpro; IPR007095; RNA_pol_DS_PS.
DR Interpro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF00771; Helicase_C_1.
DR Pfam; PF00863; Peptidase_C4_1.
DR Pfam; PF00851; Peptidase_C6_1.
DR Pfam; PF00767; Polypeptide_1.
DR Pfam; PF01577; Polypeptide_1.
DR Pfam; PF00680; RNA_dep_RNA_pol_1.
DR PRINTS; PR00966; NIAPOTPTASE.
DR SMART; SM00487; DEXDC_1.
DR SMART; SM00490; HELIC_C_1.
DR PROSITE; PS50507; RDRP_POSITIVE; 1.
DR PROSITE; PS50521; RDRP_VIRAL; 1.
KW ATP-binding; Coat protein; Helicase; Hydrolase.
SQ SEQUENCE 3072 AA; 348727 MW; F3BBA94BD96D365A CRC64;

Query Match 9.4%; Score 100; DB 12; Length 3072;
Best Local Similarity 21.5%; Pred. No. 39;
Matches 46; Conservative 38; Mismatches 72; Indels 58; Gaps 10;

QY 23 VKTESICR-----NRYTNVNVKVTKLVAN--LPKDYMTLTKVPGM-DVLSHCWISGMVY---Q 69
Db 639 IAKDGYCHINIFPAMLVNVSBDKSDFTKVRDQIMPK-----LGQWPTMLDVATAVCWYL 693
QY 70 -----ISEWVQLSDSLTDLDDKFSNISSEGLSNYSIIDKLVINVDLVECVKEN 118
Db 694 TWPFDTLSAELPRILVHKSLTMVAVLDSYGSISIG--YVYLK--ANIVSOLIFASDD 748
QY 119 SSKDLKSKSPSPRLFTPEEFRIFRNSIDAFKDFVASETSDCVSSTLSPEKDSRVS 178
Db 749 LESDLK-----FYRVGKSLTG--QVIQPTK-MLISSIVRPQMEKII 789
QY 179 VTKPFML-----PVAASLNRDSSSSNSKITYL 207
Db 790 NEPPVLVLAQSPSVLLALFNLSASLEKAVAVWL 823

RESULT 11

O19545 PRELIMINARY; PRT; 1490 AA.
AC O19545;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical 168.5 kDa protein.
GN F18C5.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;

RA None;
RT "Genome sequence of the nematode *C. elegans*: a platform for
investigating biology. The *C. elegans* Sequencing Consortium.";
RL Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Fullon L.;
RT "The sequence of *C. elegans* cosmid F18C5.";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U29097; AAA68411.1; -.
DR WormPep; F18C5.3; CE02652.
KW Hypothetical protein.
SQ SEQUENCE 1490 AA; 168480 MW; 89FF7AD689A9E668 CRC64;

Query Match 9.1%; Score 97.5; DB 5; Length 1490;
Best Local Similarity 24.4%; Pred. No. 27;
Matches 54; Conservative 28; Mismatches 82; Indels 57; Gaps 9;

QY 20 NPLVTEGICRNRYTNVKNVTKLVANLPKDYMITLKYPGMDVLPSCWISSEWVQLSD 79
DB 732 NGAVKAE--CPKAKGNRAPPEMCHLGRIVSPAGIQWLAFFRVVNEH--PSAKAVQ--- 784
QY 80 SLTDLDFKSNISEGSLNYSIID-----KLNVIVDLVECVKENSCKDLKSKFS 129
DB 785 RVSDLLSKFAG---GLKDNEISLDSQLGYIFKSLTSDIOKLEVERKNGQKDEKQGR 841
QY 130 PEERLFFPEEPRFI--FNRSIDAFKDPVVASSETSDCVSSTLSPEK-----DSRVSVTP 182
DB 842 PESCLILPAAPQRIKAGMSKVIRSRDHVFA--EFFVLLFSSLLKEKFDLSDDSMVSR 900
QY 183 FM-----LPPVAASSR 194
DB 901 FVKIILDCFPKYEKILSCSMRALSSMIOQLPAIANSQR 941

RESULT 12
Q9PQJ8 PRELIMINARY; PRT; 1447 AA.
ID 09PQJ8;
AC 09PQJ8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein U0293.
GN U0293.
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
OX NCBI_TaxID=134821;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Serovar 3;
RX MEDLINE=20500219; PubMed=11048724;
RA Glass J.J., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RA Cassell G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
urealyticum.";
RL Nature 407:757-762 (2000).
DR EMBL; AB002126; AAF30702.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 1447 AA; 167444 MW; A22A194FF79A0289 CRC64;

Query Match 9.1%; Score 97; DB 16; Length 1447;
Best Local Similarity 29.7%; Pred. No. 29;
Matches 41; Conservative 29; Mismatches 38; Indels 30; Gaps 9;
QY 17 LLENPLVKT-----EGICNRYTNVKNVTKLVANLPKDYMITLKYPGMDVLP 67
DB 17 LLENPLVKT-----EGICNRYTNVKNVTKLVANLPKDYMITLKYPGMDVLP 67

DB 351 IININAPDIKEIIRITNTSNIINNAKQODIK--QIDKIYLLIKKVLQTOFLNKS 407
QY 68 CWISEWVQLSDLTDLDK-FSN-----ISEGLSNY--SIIDKLVIYVD-----LVE 113
DB 408 AKTS--VKINFTITLIDSLFANGEIITLISNTLSNWFSSNLAKIINVEDQNSLIK 465
QY 114 CYKE--NSSKDLKSKFS 129
DB 466 PVVERFISNDLKTILKT 483

RESULT 13
Q96VK6 PRELIMINARY; PRT; 1498 AA.
ID 096VK6;
AC 096VK6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ABC transporter protein.
GN ATRE.
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MG096;
RA Andrade A.C., Braam C., Haas H., De Waard M.A.;
RT "ABC transporters and resistance to azole fungicides in the ima
mutants of *Aspergillus nidulans*.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AJ309280; CAC42216.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR001063; Ribosomal_L22.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transporter; 2.
DR SMART; SM00382; AAA_2.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
DR PROSITE; PS00464; RIBOSOMAL_L22; 1.
KW ATP-binding; Transport.
SQ SEQUENCE 1498 AA; 167675 MW; EBB9FF3F46110FEB CRC64;

Query Match 9.1%; Score 96.5; DB 3; Length 1498;
Best Local Similarity 20.4%; Pred. No. 33;
Matches 57; Conservative 35; Mismatches 88; Indels 99; Gaps 10;

QY 17 LLENPLVKT-----EGICNRYTNVKNVTKLVANLPKDYMITLK-----YVPG----- 60
DB 263 LMFSALARPNNRLGVSRSKQYAEHRDV--VMAMLGSHSTINTRVGNDPIRGVSGGERK 320
QY 61 -----MDVLPSCWISSE-----MVQLSDSLTD 83
DB 321 RVSIATATISQAPLQCDWNSGTGDSANALFECKALAMSKTGTSTACVATIQASQAYD 380
QY 84 LLDKSNISEGLSNY--SIIDKLVIIVDLVECVKENSCKDLKSKFSPEPRLF----- 135
DB 381 VFDKQTVLVEGRQIVFGNTKDAKFFVDWGFCEPRQTTADPLTSLTSPAEHLVPRYEG 440
QY 136 ----TPEEFRILFNR-----SIDAFKDPVVASSETSDCVSS- 167
DB 441 RVPCCTPDEPAAAMKSEERAKLMAIEEYERQYPIGSPYDAFVARKAMQSKORVNSP 500
QY 168 -TLSPKDSRVSVTPKPMLPVAASLRDSSSSNSKYI 205
DB 501 YTIISIQVSLCVARGF-----QRLKGFSLTITSLI 532

RESULT 14
Q9P884

ID Q9P884 PRELIMINARY; PRT; 1498 AA.
 AC Q9P884;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE ABC transporter protein.
 GN ATR1.
 OS *Emmericella nidulans* (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; *Emmericella*.
 OX NCBI_TaxID=162425;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MG096;
 RA Andrade A.C., Van Nistelrooy J.G.M., Haas H., De Waard M.A.;
 RT "ABC transporters and resistance to azole fungicides in the *ina*
 mutants of *Aspergillus nidulans*.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -|- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL; AJ276241; CAB76823.1; -;
 DR InterPro; IPR003593; AAA ATPase.
 DR InterPro; IPR003439; ABC transporter.
 DR InterPro; IPR000847; HTH_LysR.
 DR InterPro; IPR001063; Ribosomal_L22.
 DR Pfam; PF00005; ABC_tran; 2.
 DR ProDom; PD000006; ABC_transporter; 2.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
 DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
 DR PROSITE; PS00464; RIBOSOMAL_L22; 1.
 KW ATP-binding; Transport.
 SQ SEQUENCE 1498 AA; 167706 MW; AABDEA3FFD1ABFE8 CRC64;

Query Match 9.1%; Score 96.5; DB 3; Length 1498;
 Best Local Similarity 20.4%; Pred. No. 33;
 Matches 57; Conservative 35; Mismatches 88; Indels 99; Gaps 10;

QY 17 LLENPLVKT-----EGICRRVTNNVQVTKLVANLPKDYMITLK-----YVPG----- 60
 Db 263 LMSALAPARNRLBEVSRQVAHMRDV--VWAMGLSHITINRVGNDFIRGVSGERK 320
 QY 61 -----MDLPSCHWISF-----MVVQLDSPLTD 83
 Db 321 RVSIATATLSQALDQCNDSTRGLDSANALEFCNKILMSKYTGSTACVAIYQASQAYD 380
 QY 84 LDKFNSISEGLSNY--SIIDKLVINVDLVEGVKENS SKDLKSKFSPERLRF----- 135
 Db 381 VEDKVTLVLEGROIYFGNTYDADAKKFPVDMGFCEPERQTADFLTSLTSPAERLVRPGYEG 440
 QY 136 ---TPEEFRIINR-----SIDAFKDFVVASETSDCVSS- 167
 Db 441 RVPCPTDFEFAAMAKRSEERAKMAEIEYERQYPIGSPSYDAFVDAKAMQSGRQRYNSP 500
 QY 168 -TLSPKDSRVSYTKPFLPVAASSLRNDSSSSNSKYI 205
 Db 501 YTISIMQVSLCVVRGF-----QRLRGDFSLTTTSLI 532

RESULT 15
 ID Q62970 PRELIMINARY; PRT; 576 AA.
 AC Q62970;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Apolipoprotein B (Fragment).
 GN APOB.
 OS *Rattus norvegicus* (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; *Rattus*.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Liver;
 RA Shimmin L.C.;
 RT "Rattus norvegicus partial apob sequence.";
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U53873; AAA98613.1; -;
 KW Lipoprotein.
 FT NON_TER 1
 FT TER 1
 SQ SEQUENCE 576 AA; 66762 MW; FFE49CCAA69AA07A CRC64;

Query Match 8.9%; Score 94.5; DB 11; Length 576;
 Best Local Similarity 24.1%; Pred. No. 16;
 Matches 45; Conservative 35; Mismatches 64; Indels 43; Gaps 7;

QY 32 RVTNNVQVTKLVANLPKDYMITLK-----VPGMDLPSCHWISEMVVQLSD----- 79
 Db 89 RISVIEIKYTFWNLIEDPKYTEKINFRYIVRELIRY-EVDRIQVLDKSIELAHR 147
 QY 80 -SLTDLDKFSNISEGLSNYSIIDKLVINVDLVEGVKENS SKDLKSKFSPERLRF----- 127
 Db 148 YSLSEPLKLSNVLDQIEIKDYVDKLVGFIDVEMIKAVSPKNIIEELNRLIDMSVKL 207
 QY 128 KSPERLTPF-----EFRIINRSL-----DAFKDFVVASETSDCVSSSTLSPE 172
 Db 208 KAFDYHQVVDKYNKIRREMTORINAEIQALBPQKTEALKLVEDDFKTT--VNSLSLEKL 264
 QY 173 KDSRVSV 179
 Db 265 KDTKVTV 271

Search completed: February 5, 2004, 15:07:28
 Job time : 26.3526 secs

PA (AMGE-) AMGEN INC.
XX Zsebo KM, Suggs SV, Bosselman RA, Martin FH;
XX MPI: 1991-119233/17.
XX N-PSDB; AAQ11542.
XX
XX New naturally-occurring polypeptide stem cell factor analogues -
PT have haematopoietic biological activity of stem cell factor and
PT are used to treat eg leukopenia, AIDS, nerve damage and
PT infertility
XX
XX Disclosure; Fig 42; 127pp; English.
XX
XX The SCF has the ability to stimulate growth of primitive
CC progenitors including early hematopoietic progenitor cells and non-
CC hematopoietic stem cells such as neural stem cells and primordial
CC germ stem cells. The product may be used in a pharmaceutical
CC compen. for treating, in a mammal, leukopenia, thrombocytopenia,
CC anaemia, AIDS, neoplasia, nerve damage, infertility and
CC intestinal damage.
CC See also AAR11708, AAQ11509-Q11543.
XX
SQ Sequence 273 AA:

Query Match 100.0%; Score 1397; DB 12; Length 273;
Best Local Similarity 100.0%; Pred. No. 3.3e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVQDVKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVQDVKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCMISEMNVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
DB 61 MDVLPSCMISEMNVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
QY 121 KDLKSKFSKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
DB 121 KDLKSKFSKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSNRKAKNPPGDSLSLHMAAMALPALPSLIIIGFAGALYWKRR 240
DB 181 KPFMLPVAASSLRNDSSSNRKAKNPPGDSLSLHMAAMALPALPSLIIIGFAGALYWKRR 240
QY 241 QPSLTRAVENTIOINEEDNEISMLQEKEREFOEV 273
DB 241 QPSLTRAVENTIOINEEDNEISMLQEKEREFOEV 273

RESULT 2
AAR20647 ID AAR20647 standard; Protein; 273 AA.
XX
XX AAR20647;
AC
XX
DT 25-MAR-2003 (updated)
DT 30-APR-1992 (first entry)
XX
XX Human mast cell growth factor.
DE
XX
XX hMGF-2.4; hematopoietin; interleukin; IL-3; c-kit oncogene;
KM proliferation.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..25
FT /label= signal
FT 26..210
FT /label= "extracellular
FT /note= "Claimed polypeptide"
FT Region 211..237

FT FT /label= transmembrane
FT Region 238..273
FT /label= intracellular
XX
XX WO9200376-A.
XX
XX 09-JAN-1992.
XX
XX 14-JUN-1991; 91WO-US04274.
XX
XX 25-JUN-1990; 90US-0543264.
XX 10-AUG-1990; 90US-0565840.
XX 28-AUG-1990; 90US-0574152.
XX 21-SEP-1990; 90US-0586073.
XX 12-JUN-1991; 91US-0713715.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Williams DE, Lyman S;
XX
XX MPI: 1992-041558/05.
XX N-PSDB; AAQ20845.
XX
XX New isolated DNA encoding human mast cell growth factor - useful in
PT stimulating proliferation of haematopoietic cells with growth factor,
PT to treat haemolytic and hypoproliferative anaemias
XX
XX Claim 10; Fig 4; 59pp; English.
XX
XX This human MGF has a mature extracellular region of 185 amino acids.
CC There is a second form of hMGF (see AAQ20844) resulting from an
CC alternative mRNA splicing event which deletes an exon encoding an
CC additional 28 amino acids beginning at amino acid 148 of the mature
CC protein. MGF is the ligand for the protein receptor expression product
CC of the c-kit proto-oncogene. MGF can be used to augment the
CC activity of other cytokines. It can influence early lymphoid or
CC myeloid development. See also AAQ20842-3 and AAQ22204-7.
XX (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 273 AA:

Query Match 100.0%; Score 1397; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 3.3e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVQDVKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVQDVKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCMISEMNVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
DB 61 MDVLPSCMISEMNVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
QY 121 KDLKSKFSKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
DB 121 KDLKSKFSKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSNRKAKNPPGDSLSLHMAAMALPALPSLIIIGFAGALYWKRR 240
DB 181 KPFMLPVAASSLRNDSSSNRKAKNPPGDSLSLHMAAMALPALPSLIIIGFAGALYWKRR 240
QY 241 QPSLTRAVENTIOINEEDNEISMLQEKEREFOEV 273
DB 241 QPSLTRAVENTIOINEEDNEISMLQEKEREFOEV 273

RESULT 3
AAR83978 ID AAR83978 standard; Protein; 273 AA.
XX
XX AAR83978;
AC
XX
DT 25-MAR-2003 (updated)

DT 15-MAY-1996 (first entry)
 DE Human stem cell factor derived from HT1080 fibrosarcoma cell line.
 XX
 XX Stem cell factor; progenitor; hematopoiesis; SCF; anaemia;
 KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
 XX transplant; neoplasia; myelosuppression; bone marrow; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /label= sig_peptide
 FT Protein 26..248
 FT /label= mat_SCF
 XX
 XX EP676470-A1.
 XX
 XX 11-OCT-1995.
 XX
 XX 04-OCT-1990; 95EP-0105391.
 XX
 PR 01-OCT-1990; 90US-0589701.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 28-SEP-1990; 90MO-US05548.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Bosselman RA, Martin FH, Suggs SV, Zsebo KM;
 PI WPI: 1995-346090/45.
 DR N-PSDB; AAT04890.
 XX
 PT New stem cell factor polypeptide(s) - for stimulating the growth of
 PT primitive progenitor cells, esp. for treating disorders involving
 PT blood cells
 XX
 PS Claim 9; Fig 42; 127pp; English.
 XX
 XX AAR83978 is a human stem cell factor (SCF) derived from the HT1080
 CC fibrosarcoma cell line. Non-naturally occurring SCF and C-terminally
 CC truncated polypeptides, having amino acid sequences sufficiently
 CC duplicative of naturally occurring SCF, stimulate growth of primitive
 CC progenitors such as haematopoietic progenitor cells, neural stem
 CC cells and primordial germ stem cells. The peptides can be used in a
 CC composition for treating leucopenia, anaemia or thrombocytopenia,
 CC for enhancing engraftment of bone marrow during transplantation or
 CC for bone marrow recovery after chemotherapy or radiation-induced bone
 CC marrow aplasia or myelosuppression. They can also be used for
 CC treating neoplasia, nerve damage, infertility, intestinal damage or
 CC myeloproliferative disorders. Antibodies may be raised against the
 CC peptides for use in detection or neutralisation of SCF in serum. SCF
 CC may be useful for the treatment of AIDS and severe combined
 CC immunodeficiency (SCID) states alone or in combination with other
 CC factors such as IL-7.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC
 XX
 SQ Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 16; Length 273;
 Best Local Similarity 100.0%; Pred. No. 3.3e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTILTCIYLQLLFNPLVTEGICRNRVTNNVQDVKLVANLPKQDMITLKYVPG 60
 DB 1 MKKTQWTILTCIYLQLLFNPLVTEGICRNRVTNNVQDVKLVANLPKQDMITLKYVPG 60
 QY 61 MDVLPSCWISSEWVQSLTDLIDKFSNISBGLSVYSIIDKLVNIYDVLVECVKENS 120
 DB 61 MDVLPSCWISSEWVQSLTDLIDKFSNISBGLSVYSIIDKLVNIYDVLVECVKENS 120
 61 MDVLPSCWISSEWVQSLTDLIDKFSNISBGLSVYSIIDKLVNIYDVLVECVKENS 120

QY 121 KDLKKSFKSPERLFTPEEPFRIFENRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
 DB 121 KDLKKSFKSPERLFTPEEPFRIFENRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
 QY 181 KPFMLPPVAASSLRNDSSSNRKANPPGDSLSHMAALPALFSLIIGFAPGALYMKR 240
 DB 181 KPFMLPPVAASSLRNDSSSNRKANPPGDSLSHMAALPALFSLIIGFAPGALYMKR 240
 QY 241 QPSLTRAVENTIOINEDNEISMLOEKEREPQEV 273
 DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREPQEV 273
 RESULT 4
 AAW27607
 ID AAW27607 standard; Protein; 273 AA.
 XX
 XX AAW27607;
 XX
 DT 28-APR-1998 (first entry)
 XX
 DE Human recombinant stem cell factor protein.
 KW Stem cell factor; SCF; mast cell growth factor; MCGF; Steel factor;
 KW SF; SLF; analogue; treatment; haematopoietic factor; progenitor cell;
 KW pigmentation disorder; haematopoietic disorder.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..25
 FT /label= leader sequence
 FT Protein 26..274
 FT /note= "mature full length stem cell factor protein"
 XX
 XX W09738101-A1.
 XX
 PD 16-OCT-1997.
 XX
 PF 03-APR-1997; 97MO-US05541.
 XX
 PR 05-APR-1996; 96US-0628428.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Lu HS;
 XX
 DR WPI: 1997-512718/47.
 XX
 PT Stem cell factor analogue N10D or N10D/N10D - useful to treat
 PT pigmentation disorder, AIDS, nerve damage, infertility, intestinal
 PT damage or haematopoietic disorder
 XX
 PS Claim 2; Fig 1; 42pp; English.
 XX
 XX This sequence represents a membrane bound form of a human recombinant
 CC stem cell factor (SCF). Stem cell factors are also known as mast cell
 CC growth factors (MCGF) or Steel factors (SF or SLF) are haematopoietic
 CC factors which act on haematopoietic progenitor cells. Analogues of a
 CC wild type SCF sequence have been constructed (see AAW27605 and AAW27606)
 CC which have increased biological activity and stability compared to
 CC unmodified SCF and can be used treat pigmentation disorders, e.g.
 CC vitilago, acquired immunodeficiency syndrome, nerve damage, infertility,
 CC intestinal damage or a haematopoietic disorder, e.g. leucopenia,
 CC thrombocytopenia or anaemia, enhance bone marrow engraftment during
 CC transplantation or bone marrow recovery following radiation, chemical or
 CC chemotherapeutic, induced bone marrow aplasia or myelosuppression,
 CC sensitive cells to chemotherapy or mobilise peripheral blood progenitor
 CC cells. It can also be used in an in vitro haematopoietic cell, preferably
 CC bone marrow or peripheral blood progenitor cell, culture medium, where
 CC the cells are optionally subsequently transfected with exogenous DNA.
 XX
 SQ Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 18; Length 273;
 Best Local Similarity 100.0%; Pred. No. 3.3e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFNPLVKTGICRRRTNNVQVTKLVANLPKDYMTITLKYPG 60
 DB 1 MKKTQWILTCIYQLLFNPLVKTGICRRRTNNVQVTKLVANLPKDYMTITLKYPG 60
 QY 61 MDVLPSCWISSEWVQSLDSDLTDLDPKFSNISSEGLSNYSIIDLVNIYDDLVECKENSS 120
 DB 61 MDVLPSCWISSEWVQSLDSDLTDLDPKFSNISSEGLSNYSIIDLVNIYDDLVECKENSS 120
 QY 121 KDLKSKFSKSPERLFTPEEFRIENRSIDAFKDFVVASETSDCVSSSTLSPKDSRVSVT 180
 DB 121 KDLKSKFSKSPERLFTPEEFRIENRSIDAFKDFVVASETSDCVSSSTLSPKDSRVSVT 180
 QY 181 KPFLMPVVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYWKRR 240
 DB 181 KPFLMPVVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYWKRR 240
 QY 241 QPSLTRAVENIQINEEDNEISMLOEKERPEQEV 273
 DB 241 QPSLTRAVENIQINEEDNEISMLOEKERPEQEV 273

RESULT 5
 AA053284
 ID AA053284 standard; Protein; 273 AA.
 AC AA053284;
 XX 27-JUL-2000 (first entry)
 DE Human SCF protein isolated from the HT1080 fibrosarcoma cell line.
 XX Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
 KW primitive progenitor cell; haematopoietic disorder; synergistic;
 KW allogenic; autologous bone marrow transplant; gene therapy;
 KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;
 cancer.
 XX Homo sapiens.
 OS
 XX
 PN EP992579-A1.
 XX
 PD 12-APR-2000.
 XX
 PF 04-OCT-1990; 99EP-0122861.
 XX
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 28-SEP-1990; 90MO-US05548.
 PR 01-OCT-1990; 90US-0589701.
 PR 04-OCT-1990; 90EP-0310899.
 XX
 PA (AMGE-) AMGEN INC.
 PI Zsebo KM, Suggs SV, BosseJmann RA, Martin FH;
 DR WPI; 2000-259135/23.
 DR N-PSDB; AAA13714.
 XX
 PT Production of hematopoietic cells suitable for administration to a
 PT subject using progenitor cells and expanding the cells using stem cell
 PT factor -
 PS Claim 22; Fig 42; 123pp; English.
 CC A method has been developed of making haematopoietic cells suitable for
 CC administration to a subject. The method comprises: (a) obtaining
 CC haematopoietic progenitor cells from a donor; and (b) expanding the

CC cells by adding to the cells a haematopoietically effective dose of a
 CC polypeptide product having at least part of the primary structural
 CC confirmation and one or more of the biological properties of naturally
 CC occurring stem cell factor (SCF). The method is useful for stimulating
 CC primitive progenitor cells including early haematopoietic progenitor
 CC cells which are capable of maturing to erythroid, megakaryocyte,
 CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
 CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
 CC SCF is useful for treating haematopoietic disorders. The method is
 CC useful for expanding early haematopoietic progenitors in syngeneic,
 CC allogeneic or autologous bone marrow transplant. SCF is useful for
 CC enhancing the efficiency of gene therapy based on transfecting the
 CC haematopoietic stem cells. SCF is also useful for combating the
 CC myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing
 CC haematopoietic recovery after acute blood loss and as a boost to the
 CC immune system for fighting neoplasia (cancer). The present sequence
 CC represents a specifically claimed human SCF from the present invention.

SQ Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 21; Length 273;
 Best Local Similarity 100.0%; Pred. No. 3.3e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFNPLVKTGICRRRTNNVQVTKLVANLPKDYMTITLKYPG 60
 DB 1 MKKTQWILTCIYQLLFNPLVKTGICRRRTNNVQVTKLVANLPKDYMTITLKYPG 60
 QY 61 MDVLPSCWISSEWVQSLDSDLTDLDPKFSNISSEGLSNYSIIDLVNIYDDLVECKENSS 120
 DB 61 MDVLPSCWISSEWVQSLDSDLTDLDPKFSNISSEGLSNYSIIDLVNIYDDLVECKENSS 120
 QY 121 KDLKSKFSKSPERLFTPEEFRIENRSIDAFKDFVVASETSDCVSSSTLSPKDSRVSVT 180
 DB 121 KDLKSKFSKSPERLFTPEEFRIENRSIDAFKDFVVASETSDCVSSSTLSPKDSRVSVT 180
 QY 181 KPFLMPVVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYWKRR 240
 DB 181 KPFLMPVVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYWKRR 240
 QY 241 QPSLTRAVENIQINEEDNEISMLOEKERPEQEV 273
 DB 241 QPSLTRAVENIQINEEDNEISMLOEKERPEQEV 273

RESULT 6
 AA05266
 ID AA05266 standard; Protein; 273 AA.
 AC AA05266;
 XX 24-OCT-2001 (first entry)
 DE Human SCF protein isolated from the HT1080 fibrosarcoma cell line.
 XX Stem cell factor; SCF; haematopoietic progenitor cell; AIDS;
 KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
 KW hypopigmentation disorder; viral disorder; HT1080 fibrosarcoma.
 XX Homo sapiens.
 OS
 XX
 PN
 AC
 XX
 DT 24-OCT-2001 (first entry)
 DE Human SCF protein isolated from the HT1080 fibrosarcoma cell line.
 XX
 KW Human; stem cell factor; SCF; haematopoietic progenitor cell; AIDS;
 KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
 KW hypopigmentation disorder; viral disorder; HT1080 fibrosarcoma.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT 1.25 Location/Qualifiers
 FT /label= Signal_peptide
 FT Protein 26..273
 FT /label= Mature_SCF
 FT Misc-difference 97
 FT /note= "Encoded by ATT"
 FT Misc-difference 258
 FT /note= "Encoded by ATT"
 PN US6248319-B1.
 XX

PD 19-JUN-2001.
 XX 24-MAY-1995; 95US-0449653.
 XX 10-APR-1991; 91US-0684535.
 PR 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 PR 21-DEC-1993; 93US-0172329.
 XX (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSSELMAN R A.
 PA (SUGS/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
 PI WPI; 2001-407312/43.
 DR N-PSDB; AAS10461.
 XX
 PT Increasing the number of early haematopoietic progenitor cells in the
 PT peripheral blood useful for the treatment of blood disorders including
 PT Hodgkin's disease comprises the administration of human stem cell
 PT factor -
 XX
 XX Example 3; Fig 42; 210pp; English.
 PS The present sequence represents human stem cell factor (SCF). The cDNA
 CC encoding this sequence is isolated from the H1080 fibrosarcoma cell
 CC line. The sequence is described in an invention relating to novel stem
 CC cell factors, the polynucleotides encoding them and methods for
 CC producing the stem cell factors. The methods involve increasing the
 CC number of early haematopoietic progenitor cells in human peripheral
 CC blood by administering a haematopoietically effective human stem cell
 CC factor polypeptide. The methods are useful for the treatment of blood
 CC disorders, including myelofibrosis, myelocytosis, osteopetrosis,
 CC metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's
 CC disease, lymphoma, Gaucher's disease, Niemann-Pick disease, refractory
 CC anaemia, malaria, vitamin B12 and folic acid deficiency,
 CC hypopigmentation disorders i.e. piebaldism and viral induced disorders,
 CC including AIDS.
 XX
 XX Sequence 273 AA;
 SO
 Query Match 100.0%; Score 1397; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 3.3e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRRNVNKKVDTKLVANLPKDYMITLKYVPG 60
 DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRRNVNKKVDTKLVANLPKDYMITLKYVPG 60
 QY 61 MDVLPSCWISSEMVVQSDSLTDLDFKSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCWISSEMVVQSDSLTDLDFKSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KDLLKSKSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180
 DB 121 KDLLKSKSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180
 QY 181 KPFLPVAASSLNDSSSNRKAQNPQDSSILHMAAMALPALFSLITGFAFGALYWKRR 240
 DB 181 KPFLPVAASSLNDSSSNRKAQNPQDSSILHMAAMALPALFSLITGFAFGALYWKRR 240
 QY 241 QPSLTRAVENTIOINEEDNEISMLQEKREFOEV 273
 DB 241 QPSLTRAVENTIOINEEDNEISMLQEKREFOEV 273

ID AAB98357 standard; Protein; 273 AA.
 XX
 AC AAB98357;
 XX
 DT 21-AUG-2001 (first entry)
 XX
 DE Human SCF protein SEQ ID NO:49.
 XX
 XX Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
 XX gene therapy.
 XX Homo sapiens.
 OS
 PN US6207454-B1.
 XX
 PD 27-MAR-2001.
 XX
 XX 31-DEC-1998; 98US-0224681.
 PF
 XX 21-DEC-1993; 93US-0172329.
 PR 24-MAY-1995; 95US-0449653.
 PR 12-JAN-1998; 98US-0005893.
 PR 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
 PI WPI; 2001-36062/38.
 DR
 XX Enhancing efficiency of transfer of polynucleotide into a target
 PT mammalian cell in vitro, involves exposing cell that expresses a stem
 PT cell factor receptor to stem cell factor, and introducing
 PT polynucleotide into cell in vitro -
 XX
 XX Example 3; Fig 16; 210pp; English.
 PS The present invention describes a method for enhancing (B) the
 CC efficiency of transfer of a polynucleotide (I) into a target mammalian
 CC cell (II) in vitro, comprising exposing (II) that expresses a stem cell
 CC factor (SCF) receptor to a biologically active SCF, its analogue or
 CC fragment, which induces cell proliferation, and introducing (I) to (II)
 CC into the cell. The method is useful for enhancing the efficiency of the
 CC transfer of a polynucleotide into a target mammalian cell in vitro.
 CC The method is useful in gene therapy techniques. AAH41301 to AAH41364
 CC and AAB98351 to AAB98390 represent sequences used in the exemplification
 CC of the present invention.
 XX
 XX Sequence 273 AA;
 SO
 Query Match 100.0%; Score 1397; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 3.3e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRRNVNKKVDTKLVANLPKDYMITLKYVPG 60
 DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRRNVNKKVDTKLVANLPKDYMITLKYVPG 60
 QY 61 MDVLPSCWISSEMVVQSDSLTDLDFKSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCWISSEMVVQSDSLTDLDFKSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KDLLKSKSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180
 DB 121 KDLLKSKSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSVT 180
 QY 181 KPFLPVAASSLNDSSSNRKAQNPQDSSILHMAAMALPALFSLITGFAFGALYWKRR 240
 DB 181 KPFLPVAASSLNDSSSNRKAQNPQDSSILHMAAMALPALFSLITGFAFGALYWKRR 240

Db 181 KPFMLPVAASSLRNDSSSNRKAKPPGDSLSHMAAMALPALFSLITGFAGALYMKKR 240
 QY 241 QPSLTRAVENIQINEEDNEISMLQEKEREFOEV 273
 Db 241 QPSLTRAVENIQINEEDNEISMLQEKEREFOEV 273

RESULT 8
 ID AAB98367 standard; Protein; 273 AA.
 XX AAB98367;
 AC AAB98367;
 XX 21-AUG-2001 (first entry)
 DE Human SCF protein sequence SEQ ID NO:61.
 KM Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
 KW gene therapy.
 XX Homo sapiens.
 OS US6207454-B1.
 PN 27-MAR-2001.
 PD 31-DEC-1998; 98US-0224681.
 PF 21-DEC-1993; 93US-0172329.
 PR 24-MAY-1995; 95US-0449653.
 PR 12-JAN-1998; 98US-0005893.
 PR 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-042383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 XX (AMGE-) AMGEN INC.
 PA Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 PI WPI; 2001-366062/38.
 DR N-PSDB; AAH41344.
 XX Enhancing efficiency of transfer of polynucleotide into a target
 PT mammalian cell in vitro, involves exposing cell that expresses a stem
 PT cell factor receptor to stem cell factor, and introducing
 PT polynucleotide into cell in vitro -
 XX Claim 17; Fig 42; 210pp; English.
 PS The present invention describes a method for enhancing (E) the
 CC efficiency of transfer of a polynucleotide (I) into a target mammalian
 CC cell (II) in vitro, comprising exposing (II) that expresses a stem cell
 CC factor (SCF) receptor to a biologically active SCF, its analogue or
 CC fragment, which induces cell proliferation, and introducing (I) to (II)
 CC in vitro. Exposure of SCF to (II) results in increased uptake of (I)
 CC into the cell. The method is useful for enhancing the efficiency of the
 CC transfer of a polynucleotide into a target mammalian cell in vitro.
 CC The method is useful in gene therapy techniques. AAH41301 to AAH41364
 CC and AAB98351 to AAB98390 represent sequences used in the exemplification
 CC of the present invention.
 XX Sequence 273 AA;
 SQ

Query Match 100.0%; Score 1397; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 3.3e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLOLLFNPLVKTGICRNRYTNVNVKQYKLVANLPQDWTITLKYPVG 60
 DB 1 MKKTQWILTCIYLOLLFNPLVKTGICRNRYTNVNVKQYKLVANLPQDWTITLKYPVG 60

QY 61 MDVLPSCHEISEMNVQLSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYDVLVECKENSS 120
 Db 61 MDVLPSCHEISEMNVQLSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYDVLVECKENSS 120
 QY 121 KDLKKSFFSPEPRFLTTPPEFFRIENRSIDAFKDFVAVASETDCVVSSTLSPEKSRVSVT 180
 Db 121 KDLKKSFFSPEPRFLTTPPEFFRIENRSIDAFKDFVAVASETDCVVSSTLSPEKSRVSVT 180
 QY 181 KPFMLPVAASSLRNDSSSNRKAKPPGDSLSHMAAMALPALFSLITGFAGALYMKKR 240
 Db 181 KPFMLPVAASSLRNDSSSNRKAKPPGDSLSHMAAMALPALFSLITGFAGALYMKKR 240
 QY 241 QPSLTRAVENIQINEEDNEISMLQEKEREFOEV 273
 Db 241 QPSLTRAVENIQINEEDNEISMLQEKEREFOEV 273

RESULT 9
 ID AAU02460 standard; Protein; 273 AA.
 XX AAU02460;
 AC AAU02460;
 XX 29-AUG-2001 (first entry)
 DE Human SCF protein isolated from the HT1080 fibrosarcoma cell line.
 KM Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
 HT1080 fibrosarcoma.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Protein 1..25
 FT /label= Signal_peptide
 FT Protein 26..273
 FT /label= Mature_SCF
 XX US6207417-B1.
 PN 27-MAR-2001.
 PD 07-JUN-1995; 95US-0482918.
 PF 21-DEC-1993; 93US-0172329.
 PR 16-OCT-1989; 89US-042383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 XX (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 DR WPI; 2001-298941/31.
 DR N-PSDB; AAS04124.
 XX Novel nucleic acids encoding stem cell factor useful for treating
 PT disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's
 PT disease, Kala azar, anaemia and septicemia -
 XX Example 5; Fig 42A-42C; 209pp; English.
 PS The present sequence representing human SCF (stem cell factor) protein
 CC is isolated from the HT1080 fibrosarcoma cell line. The present invention
 CC relates to novel stem cell factors (AAU02453-AAU02458, AAU02461) and
 CC the polynucleotides encoding them. SCF stimulate primitive progenitor
 CC cells including early haematopoietic progenitor cells. The invention also

describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides (AAU04081-AAU04117) used in the isolation of human and rat SCF sequences. The polynucleotide encoding SCF is useful for producing SCF and useful in gene therapy. It is useful for treating disorders involving blood cells such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia, congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis, disseminated fungus disease, fulminating septicemia, malaria, vitamin B12 and folic acid deficiency, pyridoxine deficiency, and hypopigmentation disorders such as piebaldism and vitiligo.

Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 22; Length 273;
Best Local Similarity 100.0%; Pred. No. 3.3e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKKTQWILTCIYLQLLFNPVLTGICRNVTNNVKDTLVANLPKDYMITLKYVPG 60
1 MKKTQWILTCIYLQLLFNPVLTGICRNVTNNVKDTLVANLPKDYMITLKYVPG 60
61 MDVLPCHCISEMNVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
61 MDVLPCHCISEMNVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
121 KDLKKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSYT 180
121 KDLKKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSYT 180
181 KPEFMLPPVAASSLRNDSSSNRKAKNPBGDSSLHMAAAMPALFSLITGFAGALYWKRR 240
181 KPEFMLPPVAASSLRNDSSSNRKAKNPBGDSSLHMAAAMPALFSLITGFAGALYWKRR 240
241 QPSLTRAVENTIQINEEDNEISMLQEKEREFQEV 273
241 QPSLTRAVENTIQINEEDNEISMLQEKEREFQEV 273

RESULT 10

ID AAU02766 standard; Protein; 273 AA.

AC AAU02766;

DT 29-AUG-2001 (first entry)

Human SCF protein isolated from the HT1080 fibrosarcoma cell line.

Human: stem cell factor; SCF; early haematopoietic progenitor cell;
blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
HT1080 fibrosarcoma.

Homo sapiens.

Key location/Qualifiers

FT Protein 1..25 /label= Signal_peptide

FT Protein 26..273 /label= Mature_SCF

PN US6218148-B1.

PD 17-APR-2001.

PF 21-DEC-1993; 93US-0172329.

PR 25-NOV-1992; 92US-0988235.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 01-OCT-1990; 90US-0589701.

(AMGE-) AMGEN INC.

Zsebo KM, Bosseiman RA, Suggs SV, Martin FH;

WPI; 2001-281051/29.

N-PSDB; AAS04224.

Isolated DNA sequence, encoding polypeptide product useful for stimulating growth of early haematopoietic progenitor cells -

Example 5; Fig 42A-42C; 167pp; English.

The present sequence representing human SCF (stem cell factor) protein is isolated from the HT1080 fibrosarcoma cell line. The present invention relates to novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797) and the polynucleotides encoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides (AAU04182-AAU04218) used in the isolation of human and rat SCF sequences. The polynucleotide encoding SCF is useful for producing SCF and useful in gene therapy. It is useful for treating disorders involving blood cells such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia, congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis, disseminated fungus disease, fulminating septicemia, malaria, vitamin B12 and folic acid deficiency, pyridoxine deficiency, and hypopigmentation disorders such as piebaldism and vitiligo.

Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 22; Length 273;
Best Local Similarity 100.0%; Pred. No. 3.3e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKKTQWILTCIYLQLLFNPVLTGICRNVTNNVKDTLVANLPKDYMITLKYVPG 60
1 MKKTQWILTCIYLQLLFNPVLTGICRNVTNNVKDTLVANLPKDYMITLKYVPG 60
61 MDVLPCHCISEMNVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
61 MDVLPCHCISEMNVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
121 KDLKKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSYT 180
121 KDLKKSFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSYT 180
181 KPEFMLPPVAASSLRNDSSSNRKAKNPBGDSSLHMAAAMPALFSLITGFAGALYWKRR 240
181 KPEFMLPPVAASSLRNDSSSNRKAKNPBGDSSLHMAAAMPALFSLITGFAGALYWKRR 240
241 QPSLTRAVENTIQINEEDNEISMLQEKEREFQEV 273
241 QPSLTRAVENTIQINEEDNEISMLQEKEREFQEV 273

RESULT 11

ID AAB73567 standard; Protein; 273 AA.

AC AAB73567;

DT 07-AUG-2001 (first entry)

Human SCF protein isolated from the HT1080 fibrosarcoma cell line.

Human: stem cell factor; SCF; early haematopoietic progenitor cell;
blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
HT1080 fibrosarcoma.

```

OS Homo sapiens.
XX Key
XX Location/Qualifiers
FH Protein 1..25
FT /label= Signal_peptide
FT 26..273
FT Protein /label= Mature_SCF
XX
XX US6204363-B1.
XX
XX 20-MAR-2001.
XX
XX 25-NOV-1992; 92US-0982255.
XX
XX 10-APR-1991; 91US-0684535.
XX 16-OCT-1989; 89US-0422383.
XX 11-JUN-1990; 90US-0537198.
XX 24-AUG-1990; 90US-0573616.
XX 01-OCT-1990; 90US-0589701.
XX
XX (AMGE-) AMGEN INC.
XX
XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
XX WPI; 2001-256683/26.
XX N-PSDB; AAH23901.
XX
XX New stem cell factor polypeptides and their analogs which stimulate
XX growth of early hematopoietic progenitors, useful for treating aplastic
XX anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
XX disease
XX
XX Claim 7; Fig 42A-42C; 166pp; English.
XX
XX The present sequence representing human SCF (stem cell factor) protein
XX is isolated from the HT1080 fibrosarcoma cell line. The present
XX invention relates to novel stem cell factors
XX (AAH23561-AAH73568, AAH73571-AAH73576) and the polynucleotides
XX encoding them. SCF stimulate primitive progenitor cells including early
XX hematopoietic progenitor cells. The invention also describes SCF
XX peptides (AAH73578-AAH73597) and the oligonucleotides
XX (AAH23859-AAH23895) used in the isolation of human and rat SCF
XX sequences. The polynucleotide encoding SCF is useful for producing
XX SCF and useful in gene therapy. It is useful for treating disorders
XX involving blood cells such as myelofibrosis, metastatic carcinoma,
XX acute leukemia, multiple myeloma, Hodgkin's disease, lymphoma,
XX Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
XX sarcoidosis, military tuberculosis, disseminated fungus disease,
XX fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
XX pyridoxine deficiency, and hypopigmentation disorders such as
XX piebaldism and vitiligo.
XX
XX Sequence 273 AA:
SQ

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Query Match 100.0%; Score 1397; DB 22; Length 273;
Best Local Similarity 100.0%; Pred. No. 3.3e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MKKTQWIIITCIYQLLLFNPLVKTGICRNRVTNNVDYTKLVANLPRDYMITLKYVVG 60
DB 1 MKKTQWIIITCIYQLLLFNPLVKTGICRNRVTNNVDYTKLVANLPRDYMITLKYVVG 60
QY 61 MOVLPBHCWISSEWVQLSDSLTDLDFKFSNISGLSNYSIIDKLVINIVDVLVCVKNSS 120
DB 61 MOVLPBHCWISSEWVQLSDSLTDLDFKFSNISGLSNYSIIDKLVINIVDVLVCVKNSS 120
QY 121 KDLKSFKSPPEPLFTPEEPFRIFNRSIDAFKDFVVAASEPDCVVSSTLSPKDSRVST 180
DB 121 KDLKSFKSPPEPLFTPEEPFRIFNRSIDAFKDFVVAASEPDCVVSSTLSPKDSRVST 180
QY 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSSLHMAAALPALFSLIIFAGALYMKR 240
DB 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSSLHMAAALPALFSLIIFAGALYMKR 240
QY 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSSLHMAAALPALFSLIIFAGALYMKR 240
DB 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSSLHMAAALPALFSLIIFAGALYMKR 240

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QY 241 QPSTRAVENIOINEDNEISMLQKEREPOEV 273
DB 241 QPSTRAVENIOINEDNEISMLQKEREPOEV 273
RESULT 12
ID AAB96941 standard; Protein; 273 AA.
XX AAB96941;
XX
XX 13-JUL-2001 (first entry)
XX
XX Human stem cell factor SEQ ID NO: 48.
XX
XX Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
XX gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
XX neurological damage; intestinal damage; infertility; AIDS; SCID;
XX severe combined immunodeficiency.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Protein 1..25
FT /label= signal_peptide
FT 26..273
FT Protein /label= mature_stem_cell_factor
XX
XX US6207802-B1.
XX
XX 27-MAR-2001.
XX
XX 09-NOV-1994; 94US-0336728.
XX
XX 25-NOV-1992; 92US-0982255.
XX 16-OCT-1989; 89US-0422383.
XX 11-JUN-1990; 90US-0537198.
XX 24-AUG-1990; 90US-0573616.
XX 01-OCT-1990; 90US-0589701.
XX
XX (AMGE-) AMGEN INC.
XX
XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
XX WPI; 2001-353108/37.
XX N-PSDB; AAF89102.
XX
XX Novel isolated non-human mammalian stem cell factor polypeptide
XX stimulating growth of early hematopoietic progenitor cells, useful for
XX treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,
XX sarcoidosis
XX
XX Disclosure; Fig 15D; 209pp; English.
XX
XX The present invention provides the protein and coding sequences of
XX mammalian stem cell factors (SCFs). These are capable of stimulating the
XX growth of early hematopoietic progenitor cells, neural stem cells and
XX primordial germ stem cells. The sequences are useful in the treatment of
XX leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
XX nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
XX and intestinal damage, infertility, AIDS and severe combined
XX immunodeficiency (SCID). The present sequence is an SCF described in the
XX invention.
XX
XX Sequence 273 AA:
SQ

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Query Match 100.0%; Score 1397; DB 22; Length 273;
Best Local Similarity 100.0%; Pred. No. 3.3e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MKKTQWIIITCIYQLLLFNPLVKTGICRNRVTNNVDYTKLVANLPRDYMITLKYVVG 60

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Db 1 MKKTQTWILTCIYLQLLFNPVLTGEGICRRVTNNVDYTKLVANLPKDYMITLKYVPG 60
 QY 61 MDVLPSCWISWVQVQLSDSLTDLIDKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 Db 61 MDVLPSCWISWVQVQLSDSLTDLIDKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KDLKKSFKSPERPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
 Db 121 KDLKKSFKSPERPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
 QY 181 KPFTMLPPVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240
 Db 181 KPFTMLPPVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240
 QY 241 QPSLTRAVENTIQINEEDNEISMLQEKERPEOV 273
 Db 241 QPSLTRAVENTIQINEEDNEISMLQEKERPEOV 273

RESULT 13

AAB96942
 ID AAB96942 standard; Protein; 273 AA.
 AC AAB96942;

DT 13-JUL-2001 (first entry)

DE Human stem cell factor SEQ ID NO: 49.

KW Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
 gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
 neurological damage; intestinal damage; infertility; AIDS; SCID;
 severe combined immunodeficiency.

OS Homo sapiens.

PN US6207802-B1.

PD 27-MAR-2001.

PF 09-NOV-1994; 94US-0336728.

PR 25-NOV-1992; 92US-0982255.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 01-OCT-1990; 90US-0589701.

PA (AMGE-) AMGEN INC.

PI Zsebo KM, Bosseelman RA, Suggs SV, Martin FH;

DR WPI; 2001-353108/37.

PT Novel isolated non-human mammalian stem cell factor polypeptide
 stimulating growth of early haematopoietic progenitor cells, useful for
 treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,
 sarcoïdosis -

PS Example 3; Fig 16; 209pp; English.

CC The present invention provides the protein and coding sequences of
 mammalian stem cell factors (SCFs). These are capable of stimulating the
 growth of early haematopoietic progenitor cells, neural stem cells and
 primordial germ stem cells. The sequences are useful in the treatment of
 leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
 nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
 and intestinal damage, infertility, AIDS and severe combined
 immunodeficiency (SCID). The present sequence is an SCF described in the
 invention.

CC Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 3.3e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKTQTWILTCIYLQLLFNPVLTGEGICRRVTNNVDYTKLVANLPKDYMITLKYVPG 60
 Db 1 MKKTQTWILTCIYLQLLFNPVLTGEGICRRVTNNVDYTKLVANLPKDYMITLKYVPG 60
 QY 61 MDVLPSCWISWVQVQLSDSLTDLIDKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 Db 61 MDVLPSCWISWVQVQLSDSLTDLIDKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KDLKKSFKSPERPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
 Db 121 KDLKKSFKSPERPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180
 QY 181 KPFTMLPPVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240
 Db 181 KPFTMLPPVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240
 QY 241 QPSLTRAVENTIQINEEDNEISMLQEKERPEOV 273
 Db 241 QPSLTRAVENTIQINEEDNEISMLQEKERPEOV 273

RESULT 14

AAB96952
 ID AAB96952 standard; Protein; 273 AA.

AC AAB96952;

DT 13-JUL-2001 (first entry)

DE Human stem cell factor SEQ ID NO: 61.

KW Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
 gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
 neurological damage; intestinal damage; infertility; AIDS; SCID;
 severe combined immunodeficiency.

OS Homo sapiens.

PN US6207802-B1.

PD 27-MAR-2001.

PF 09-NOV-1994; 94US-0336728.

PR 25-NOV-1992; 92US-0982255.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 01-OCT-1990; 90US-0589701.

PA (AMGE-) AMGEN INC.

PI Zsebo KM, Bosseelman RA, Suggs SV, Martin FH;

DR WPI; 2001-353108/37.

DR N-PSDB; AAF89104.

PT Novel isolated non-human mammalian stem cell factor polypeptide
 stimulating growth of early haematopoietic progenitor cells, useful for
 treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,
 sarcoïdosis -

PS Example 3; Fig 42; 209pp; English.

XX The present invention provides the protein and coding sequences of
 CC mammalian stem cell factors (SCFs). These are capable of stimulating the
 CC growth of early haematopoietic progenitor cells, neural stem cells and
 CC primordial germ stem cells. The sequences are useful in the treatment of
 CC leukemias, haematopoietic disorders, aplastic anaemia, paroxysmal
 CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
 CC and intestinal damage, infertility, AIDS and severe combined
 CC immunodeficiency (SCID). The present sequence is an SCF described in the
 CC invention.

XX Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 3.3e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
 DB 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
 QY 61 MDVLPBHCWISBMVVOQLSDSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120
 DB 61 MDVLPBHCWISBMVVOQLSDSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120

QY 121 KDLKSFSPERPLFTPEEPFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKDSRVSVT 180
 DB 121 KDLKSFSPERPLFTPEEPFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKDSRVSVT 180
 QY 181 KPFLMPVVAASSLRDSSSNRKAKNPPGDDSLHMAAMALPALFSLIIGFAGALYMKR 240
 DB 181 KPFLMPVVAASSLRDSSSNRKAKNPPGDDSLHMAAMALPALFSLIIGFAGALYMKR 240

QY 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 273
 DB 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 273

RESULT 15

ABG95642
 ID ABG95642 standard; Protein; 273 AA.

AC ABG95642;

DT 05-DEC-2002 (first entry)

DE Human SCF protein from HT1080 fibrosarcoma cell line.

XX Stem cell factor; SCF; blood-forming system; blood cell disorder;
 KW haematopoietic system; metastatic carcinoma; acute leukaemia;
 KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
 KW refractory erythroblastic anaemia; military tuberculosis; cytostatic;
 KW disseminated fungus disease; haematopoietic; tuberculosis;
 KW antianaemic; antifungal; antimetastatic; dermatological; human;
 KW HT1080 fibrosarcoma cell line.

OS Homo sapiens.

XX EPI241258-A2.

PD 18-SEP-2002.

PF 04-OCT-1990; 2002EP-0008587.

XX 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 28-SEP-1990; 90WO-US05548.

PR 01-OCT-1990; 90US-0589701.

PR 04-OCT-1990; 90EP-0310899.

PR 04-OCT-1990; 95EP-0105391.

PA (AMGE-) AMGEN INC.

XX Zeebo KM, Suggs SV, Bosselman RA, Martin FH;
 PI WPI: 2002-684093/74.
 DR N-PSDB; ABS73859.

XX Production of a human stem cell factor (SCF) polypeptide for treating
 PT disorders involving blood cells, such as leukaemia, comprises culturing
 PT mammalian cells comprising non-human SCF promoter DNA linked to DNA
 PT encoding the human SCF -
 XX Example 16; Fig 42; 120pp; English.

XX The present invention relates to novel stem cell factors (SCFs),
 CC polynucleotide sequences encoding the SCFs, and methods of producing
 CC them. SCFs are involved in the blood-forming (haematopoietic)
 CC system in mammals, particularly humans. The method of the invention
 CC is useful for the production of human SCF. The stem cell factors are
 CC useful to treat disorders involving blood cells e.g. metastatic
 CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
 CC lymphoma, refractory erythroblastic anaemia, military tuberculosis,
 CC disseminated fungus disease, malaria, and vitiligo. The present
 CC sequence represents human SCF protein isolated from the HT1080
 CC fibrosarcoma cell line.

XX Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 23; Length 273;
 Best Local Similarity 100.0%; Pred. No. 3.3e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60

DB 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60

QY 61 MDVLPBHCWISBMVVOQLSDSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120

DB 61 MDVLPBHCWISBMVVOQLSDSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120

QY 121 KDLKSFSPERPLFTPEEPFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKDSRVSVT 180

DB 121 KDLKSFSPERPLFTPEEPFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKDSRVSVT 180

QY 181 KPFLMPVVAASSLRDSSSNRKAKNPPGDDSLHMAAMALPALFSLIIGFAGALYMKR 240

DB 181 KPFLMPVVAASSLRDSSSNRKAKNPPGDDSLHMAAMALPALFSLIIGFAGALYMKR 240

QY 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 273

DB 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFOEV 273

Search completed: February 5, 2004, 15:05:14
 Job time : 40.1074 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 5, 2004, 15:03:24 ; Search time 14.2693 Seconds
(without alignments)
808.360 Million cell updates/sec

Title: US-09-224-683-61

Perfect score: 1397
Sequence: 1 MKKTQWILTCIYLQLLFN.....NEEDNEISWLGKREPOEV 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1397	100.0	273	1	US-08-220-379B-2
2	1397	100.0	273	2	US-08-628-428-9
3	1397	100.0	273	3	US-08-482-918-49
4	1397	100.0	273	3	US-08-482-918-61
5	1397	100.0	273	3	US-09-224-681-49
6	1397	100.0	273	3	US-09-224-681-61
7	1397	100.0	273	3	US-08-336-728A-48
8	1397	100.0	273	3	US-08-336-728A-49
9	1397	100.0	273	3	US-08-336-728A-61
10	1397	99.6	273	3	US-08-482-918-48
11	1392	99.6	273	3	US-09-224-681-48
12	1381	98.9	273	3	US-08-482-918-50
13	1381	98.9	273	3	US-09-224-681-50
14	1378	98.6	273	3	US-08-336-728A-50
15	1265	90.6	248	2	US-08-955-848A-82
16	1232.5	88.2	266	3	US-08-482-918-57
17	1232.5	88.2	266	3	US-09-224-681-57
18	1232.5	88.2	266	3	US-08-336-728A-57
19	1231	88.1	245	3	US-08-482-918-63
20	1231	88.1	245	3	US-09-224-681-63
21	1231	88.1	245	3	US-08-336-728A-63
22	1202.5	86.1	274	3	US-08-336-728A-52
23	1180.5	84.5	274	3	US-08-482-918-51
24	1180.5	84.5	274	3	US-09-224-681-51
25	1180.5	84.5	274	3	US-08-336-728A-51
26	1179.5	84.4	271	3	US-08-482-918-52
27	1179.5	84.4	271	3	US-09-224-681-52

28	1178.5	84.4	274	3	US-08-336-728A-53	Sequence 53, Appl
29	1173	84.0	273	3	US-08-482-918-53	Sequence 53, Appl
30	1173	84.0	273	3	US-09-224-681-53	Sequence 53, Appl
31	1158	82.9	273	3	US-08-482-918-42	Sequence 42, Appl
32	1158	82.9	273	3	US-09-224-681-42	Sequence 42, Appl
33	1158	82.9	273	3	US-08-336-728A-42	Sequence 42, Appl
34	1158	82.9	273	3	US-08-336-728A-54	Sequence 54, Appl
35	1157	82.8	273	1	US-08-220-379B-6	Sequence 6, Appl
36	1157	82.8	273	3	US-08-482-918-55	Sequence 55, Appl
37	1157	82.8	273	3	US-09-224-681-55	Sequence 55, Appl
38	1157	82.8	273	3	US-08-336-728A-55	Sequence 55, Appl
39	1151	82.4	273	3	US-08-482-918-54	Sequence 54, Appl
40	1151	82.4	273	3	US-09-224-681-54	Sequence 54, Appl
41	1144	81.9	273	3	US-08-341-456A-11	Sequence 11, Appl
42	1144	81.9	273	2	US-08-478-414A-11	Sequence 11, Appl
43	1144	81.9	273	3	US-08-325-240A-11	Sequence 11, Appl
44	1144	81.9	273	3	US-08-898-982-11	Sequence 11, Appl
45	1144	81.9	273	4	US-09-371-261-11	Sequence 11, Appl

ALIGNMENTS

```
RESULT 1
US-08-220-379B-2
; Sequence 2, Application US/08220379B
; Patent No. 5525708
; GENERAL INFORMATION:
; APPLICANT: No. 5525708ka, Karl
; APPLICANT: Lobell, Robert B
; TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/220,379B
; FILING DATE: 28-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr, James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Cytowed/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; NAME/KEY: cleavage site
; LOCATION: 164..165
; US-08-220-379B-2

Query Match      100.0%; Score 1397; DB 1; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.9e-134; Indels 0; Gaps 0;
Matches 273; Conservative 0; Mismatches 0;

QY      1 MKKTQWILTCIYLQLLFNPLVKTEGICRRRVTVNNVQVTKLVANLPKQWITLTKYVG 60
DB      1 MKKTQWILTCIYLQLLFNPLVKTEGICRRRVTVNNVQVTKLVANLPKQWITLTKYVG 60
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Db	61	MDVLSSHCHISSEWVVO	QSLTDL	LPKFNISG	LSNYSL	IDLXVNI	VDDLV	CEK	ENSS	120
Qy	121	KDLKKSFKSP	PEPRLFT	PEEFPR	IFN	SDA	FKQFV	VA	SE	180
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1      RESULT 2
2      US-08-628-428-9
3      ; Sequence 9, Application US/08628428
4      ; Patent No. 5883962
5      ;
6      ; GENERAL INFORMATION:
7      ; APPLICANT: Lu, Hsieng
8      ; TITLE OF INVENTION: SCF ANALOG COMPOSITIONS AND METHODS
9      ; NUMBER OF SEQUENCES: 9
10     ; CORRESPONDENCE ADDRESS:
11     ; ADDRESSEE: Amgen Inc.
12     ; STREET: 1840 DeHavilland Drive
13     ; CITY: Thousand Oaks
14     ; STATE: CA
15     ; COUNTRY: USA
16     ; ZIP: 91320-1789
17     ;
18     ; COMPUTER READABLE FORM:
19     ; MEDIUM TYPE: Floppy disk
20     ; COMPUTER: IBM PC compatible
21     ; OPERATING SYSTEM: PC-DOS/MS-DOS
22     ; SOFTWARE: Patentin Release #1.0, Version #1.30
23     ; CURRENT APPLICATION DATA:
24     ; APPLICATION NUMBER: US/08/628,428
25     ; FILING DATE: 05-APR-1996
26     ;
27     ; CLASSIFICATION: 435
28     ; ATTORNEY/AGENT INFORMATION:
29     ; NAME: Knight, Matthew W
30     ; REGISTRATION NUMBER: 36,846
31     ; REFERENCE/DOCKET NUMBER: A-400
32     ;
33     ; INFORMATION FOR SEQ ID NO: 9:
34     ; SEQUENCE CHARACTERISTICS:
35     ;     LENGTH: 273 amino acids
36     ;     TYPE: amino acid
37     ;     STRANDEDNESS: single
38     ;     TOPOLOGY: linear
39     ;
40     ; MOLECULE TYPE: protein
41     ;
42     ; FEATURE:
43     ; NAME/KEY: Protein
44     ; LOCATION: 1..273
45     ; OTHER INFORMATION:
46     ; OTHER INFORMATION:
47     ; OTHER INFORMATION:
48     ; OTHER INFORMATION:
49     ;
50     ; US-08-628-428-9

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	Query March	100.0%;	Score 1397;	DB 2;	Length 273;
	Best Local Similarity	100.0%;	Pred. No. 2.9e-13;		
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Oy	61 MDVLPSHCWISSENVVOQLSDSLFTDLLDPKESINISEGSNSYSIIIDKLVINIYVDLPECVKENSS	120			
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QY	121	KDLKSKFKSEPEPLFTPEEFERIRNRSIDAFQDFVASETSDCVVSTLSPEKORSVVT	180
Db	121	KDLKSKFKSEPEPLFTPEEFERIRNRSIDAFQDFVASETSDCVVSTLSPEKORSVVT	180
QY	181	KPEMLPVAASSLRNDSSSNRKANPPGDSSLHMAAMALPALPSLITGFAGALYWKRR	240
Db	181	KPEMLPVAASSLRNDSSSNRKANPPGDSSLHMAAMALPALPSLITGFAGALYWKRR	240
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```

1      RESULT 3
2      US-08-482-918-49
3      ; Sequence 49, Application US/08482918
4      Patent No. 6207417
5      GENERAL INFORMATION:
6      APPLICANT: Zsebo, Krisztina M.
7      APPLICANT: Bosselman, Robert A.
8      APPLICANT: Suggs, Sidney V.
9      APPLICANT: Martin, Francis H.
10     TITLE OF INVENTION: Stem Cell Factor
11     NUMBER OF SEQUENCES: 104
12     CORRESPONDENCE ADDRESS:
13     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
14     STREET: 6300 Sears Tower, 233 South Wacker Drive
15     CITY: Chicago
16     STATE: Illinois
17     COUNTRY: United States of America
18     ZIP: 60606-6402
19     COMPUTER READABLE FORM:
20     MEDIUM TYPE: floppy disk
21     COMPUTER: IBM PC compatible
22     OPERATING SYSTEM: PC-DOS/MS-DOS
23     SOFTWARE: PatentIn Release #1.0, Version #1.30
24     CURRENT APPLICATION DATA:
25     APPLICATION NUMBER: US/08/482,918
26     FILING DATE: 07-JUN-1995
27     CLASSIFICATION: 424
28     ATTORNEY/AGENT INFORMATION:
29     NAME: Clough, David W.
30     REGISTRATION NUMBER: 36,107
31     REFERENCE/DOCKET NUMBER: 01017/33005
32     TELECOMMUNICATION INFORMATION:
33     TELEPHONE: 312/474-6300
34     TELEFAX: 312/474-0448
35     TELEX: 25-3856
36     INFORMATION FOR SEQ ID NO: 49:
37     SEQUENCE CHARACTERISTICS:
38     LENGTH: 273 amino acids
39     TYPE: amino acid
40     STRANDEDNESS: single
41     TOPOLOGY: linear
42     MOLECULE TYPE: protein
43     ; US-08-482-918-49

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Query Match	100.0%	Score 1397	DB 3	Length 273
Best Local Similarity	100.0%	Pred. No. 2.9e-134		
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Db	61	MDVLPESHCHISMVVQLSDSLTDLDDKFSNISEGLSNYSIIIDKLVNIVDLVLCVKNSS	120
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Db		181	KPFMLPPVAASLRNDSSSNRKANKNPEDSSLHMAAMALPALFSLITIGFAFGALYWKRR	240
QY		241	QPSLTRAVENTIQINEDNEISMLOEKEREFECEV	273
Db		241	QPSLTRAVENTIQINEDNEISMLOEKEREFCEV	273
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			Sequence 61, Application US/08482918	
			Patent No. 6207417	
			GENERAL INFORMATION:	
			APPLICANT: Zeebo, Kristina M.	
			APPLICANT: Bosselman, Robert A.	
			APPLICANT: Suggs, Sidney V.	
			APPLICANT: Martin, Francis H.	
			TITLE OF INVENTION: Stem Cell Factor	
			NUMBER OF SEQUENCES: 104	
			CORRESPONDENCE ADDRESS:	
			ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun	
			STREET: 6300 Sears Tower, 233 South Wacker Drive	
			CITY: Chicago	
			STATE: Illinois	
			COUNTRY: United States of America	
			ZIP: 60606-6402	
			COMPUTER READABLE FORM:	
			MEDIUM TYPE: Floppy disk	
			COMPUTER: IBM PC compatible	
			OPERATING SYSTEM: PC-DOS/MS-DOS	
			SOFTWARE: Patent Release #1.0, Version #1.30	
			CURRENT APPLICATION DATA:	
			APPLICATION NUMBER: US/08/482, 918	
			FILING DATE: 07-JUN-1995	
			CLASSIFICATION: 424	
			ATTORNEY/AGENT INFORMATION:	
			NAME: Clough, David W.	
			REGISTRATION NUMBER: 36,107	
			REFERENCE/DOCKET NUMBER: 01017/33005	
			TELECOMMUNICATION INFORMATION:	
			TELEPHONE: 312/474-6300	
			TELEFAX: 312/474-0448	
			TELEX: 25-3856	
			INFORMATION FOR SEQ ID NO: 61:	
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			US-08-482-918-61	
			Query Match	
			Best Local Similarity 100.0%; Score 1397; DB 3; Length 273;	
			Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY		1	MKKTOTWILTCYIQLLLFNPLVKTEGICRNRVTNNVKKVTKLVANLPKDYMTLTLYVP	60
Db		1	MKTQTWILTCYIQLLLFNPLVKTEGICRNRVTNNVKKVTKLVANLPKDYMTLTLYVP	60
QY		61	MDVLPSHCWISSENVVQLSDSLTDLDKFSNISSEGLSNYSIIDKLAVNIIVDLVECVKENNS	120
Db		61	MDVLPSHCWISSENVVQLSDSLTDLDKFSNISSEGLSNYSIIDKLAVNIIVDLVECVKENNS	120
QY		121	KDLKSFKSPPEPRLFTPEEPFRIFNRSIDAFCDFVAASETDCVASTSPEKDSRVSVT	180
Db		121	KDLKSFKSPPEPRLFTPEEPFRIFNRSIDAFKDFVAASETDCVASTLSPEKDSRVSVT	180
QY		181	KPFMLPPVAASLRNDSSSNRKANKNPEDSSLHMAAMALPALFSLITIGFAFGALYWKRR	240
Db		181	KPFMLPPVAASLRNDSSSNRKANKNPEDSSLHMAAMALPALFSLITIGFAFGALYWKRR	240

```

241 OPSITRAVENIQTINEEDNEISMLQEKERPEQV 273
Db 241 OPSITRAVENIQTINEEDNEISMLQEKERPEQV 273

RESULT 5
US-09-224-681-49
; Sequence 49, Application US/09224681
; Patent No. 6207454
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
; TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,681
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,893
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/35199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TEXT:
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-224-681-49

```

Query Match 100.0%; Score 1397; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.9e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVQDVKLVANLPKDYMTLTKYVG 60
DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVQDVKLVANLPKDYMTLTKYVG 60

QY 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120

QY 121 KDLKSFSPKSPRLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPEKDSRVSVT 180
DB 121 KDLKSFSPKSPRLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPEKDSRVSVT 180

QY 181 KPFLMPVVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240
DB 181 KPFLMPVVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240

QY 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFEV 273

RESULT 6
US-09-224-681-61
Sequence 61, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-224-681-61

Query Match 100.0%; Score 1397; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.9e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVQDVKLVANLPKDYMTLTKYVG 60
DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVQDVKLVANLPKDYMTLTKYVG 60

QY 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120

QY 121 KDLKSFSPKSPRLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPEKDSRVSVT 180
DB 121 KDLKSFSPKSPRLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPEKDSRVSVT 180

QY 181 KPFLMPVVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240
DB 181 KPFLMPVVAASSLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYMKR 240

QY 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLQEKEREFEV 273

RESULT 7
US-08-336-728A-48
Sequence 48, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255

FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEO ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-48

Query Match 100.0%; Score 1397; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.9e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKTQWILTCIYLLFNPVLYKTEGICRNRTNNKVDYKLVANLPKDYMTITLKYPG 60
DB 1 MKKTQWILTCIYLLFNPVLYKTEGICRNRTNNKVDYKLVANLPKDYMTITLKYPG 60
QY 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEKENS 120
DB 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEKENS 120
QY 121 KDLKSKFSPEPRLFTPEEFPRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKSKFSPEPRLFTPEEFPRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVSVT 180
QY 181 KPPMLPPVAASLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYWK 240
DB 181 KPPMLPPVAASLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYWK 240
QY 241 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 273
DB 241 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 273

RESULT 8
US-08-336-728A-49
Sequence 49, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEO ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-49

Query Match 100.0%; Score 1397; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.9e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKTQWILTCIYLLFNPVLYKTEGICRNRTNNKVDYKLVANLPKDYMTITLKYPG 60
DB 1 MKKTQWILTCIYLLFNPVLYKTEGICRNRTNNKVDYKLVANLPKDYMTITLKYPG 60
QY 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEKENS 120
DB 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVCEKENS 120
QY 121 KDLKSKFSPEPRLFTPEEFPRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKSKFSPEPRLFTPEEFPRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVSVT 180
QY 181 KPPMLPPVAASLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYWK 240
DB 181 KPPMLPPVAASLRNDSSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYWK 240
QY 241 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 273
DB 241 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 273

RESULT 9
US-08-336-728A-61
Sequence 61, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.

APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/569,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/557,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-61

Query Match 100.0%; Score 1397; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.9e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLFNPLVKTGICRRVTNNVQDVTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWTLTCTIYQLLFNPLVKTGICRRVTNNVQDVTKLVANLPKDYMITLKYVPG 60

QY 61 MDVLP SHCWISEMVOVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVINIYVDLVECKENSS 120
DB 61 MDVLP SHCWISEMVOVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVINIYVDLVECKENSS 120

QY 121 KDLKSFSPRPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
DB 121 KDLKSFSPRPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180

QY 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSLHMAAMALPALFSLIIGFAGALYMKR 240
DB 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSLHMAAMALPALFSLIIGFAGALYMKR 240

QY 241 QPSLTRAVENTIQINEEDNEISMLOEKERFQEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKERFQEV 273

RESULT 10
US-08-482-918-48
Sequence 48, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-48

Query Match 99.6%; Score 1392; DB 3; Length 273;
Best Local Similarity 99.6%; Pred. No. 9.5e-134;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLFNPLVKTGICRRVTNNVQDVTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWTLTCTIYQLLFNPLVKTGICRRVTNNVQDVTKLVANLPKDYMITLKYVPG 60

QY 61 MDVLP SHCWISEMVOVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVINIYVDLVECKENSS 120
DB 61 MDVLP SHCWISEMVOVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVINIYVDLVECKENSS 120

QY 121 KDLKSFSPRPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
DB 121 KDLKSFSPRPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180

QY 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSLHMAAMALPALFSLIIGFAGALYMKR 240
DB 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSLHMAAMALPALFSLIIGFAGALYMKR 240

QY 241 QPSLTRAVENTIQINEEDNEISMLOEKERFQEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKERFQEV 273

RESULT 11
US-09-224-681-48
Sequence 48, Application US/09224681

Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-48
Query Match 99.6%; Score 1392; DB 3; Length 273;
Best Local Similarity 99.6%; Pred. No. 9.5e-134;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVKDVTKLVANLPKDYMITLKVVG 60
DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVKDVTKLVANLPKDYMITLKVVG 60
QY 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECKENSS 120

DB 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECKENSS 120
QY 121 KOLKSFSPSPRLTPEEPFRIFNRSIDAFDPVAVSETSCVVSSTLSPKDSRVST 180
DB 121 KOLKSFSPSPRLTPEEPFRIFNRSIDAFDPVAVSETSCVVSSTLSPKDSRVST 180
QY 181 KPFMLPVAASSLRNDSSSNRKAQPGDSSLHMAALPALFSLIIGFAGALYMKR 240
DB 181 KPFMLPVAASSLRNDSSSNRKAQPGDSSLHMAALPALFSLIIGFAGALYMKR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLQEKEREPQEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLQEKEREPQEV 273
RESULT 12
US-08-482-918-50
Sequence 50, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-50
Query Match 98.9%; Score 1381; DB 3; Length 273;
Best Local Similarity 98.9%; Pred. No. 1.3e-132;
Matches 270; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVKDVTKLVANLPKDYMITLKVVG 60
DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRVTNNVKDVTKLVANLPKDYMITLKVVG 60
QY 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECKENSS 120
DB 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECKENSS 120
QY 121 KOLKSFSPSPRLTPEEPFRIFNRSIDAFDPVAVSETSCVVSSTLSPKDSRVST 180

|||||
121 KDLKKSFKSPERLFTPEEFRIFNRSIDAFKDFAVASSTDCVVSSTLSPEKDSHVT 180
QY 181 KPFLPVAASLRNDSSSNRKAKNPPGSSLHWAAMLPALFSLIIGFAGALYMKR 240
DB 181 KPFLPVAASLRNDSSSNRKAKNPPGSSLHWAAMLPALFSLIIGFAGALYMKR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 13
US-09-224-681-50
; Sequence 50, Application US/09224681
; Patent No. 6207454
; GENERAL INFORMATION:
; APPLICANT: Zeebo, Kristina M.
; APPLICANT: Bosseiman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
; TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,681
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,893
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/35199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-50

Query Match 98.9%; Score 1381; DB 3; Length 273;
Best Local Similarity 98.9%; Pred. No. 1.3e-133;
Matches 270; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRRRVTVNNVQVTKLVANLPKDYMTLKYYVG 60
DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRRRVTVNNVQVTKLVANLPKDYMTLKYYVG 60
QY 61 MDVLPSCWISSEMVQVSDSLTDLLDKPSNISSEGSNTSIIDKLVNIYVDLVECKENSS 120
DB 61 MDVLPSCWISSEMVQVSDSLTDLLDKPSNISSEGSNTSIIDKLVNIYVDLVECKENSS 120
QY 121 KDLKKSFKSPERLFTPEEFRIFNRSIDAFKDFVAVASSTDCVVSSTLSPEKDSRVSVT 180
DB 121 KDLKKSFKSPERLFTPEEFRIFNRSIDAFKDFVAVASSTDCVVSSTLSPEKDSRVSVT 180
QY 181 KPFLPVAASLRNDSSSNRKAKNPPGSSLHWAAMLPALFSLIIGFAGALYMKR 240
DB 181 KPFLPVAASLRNDSSSNRKAKNPPGSSLHWAAMLPALFSLIIGFAGALYMKR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 14
US-08-336-728A-50
; Sequence 50, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: Zeebo, Kristina M.
; APPLICANT: Bosseiman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,728A
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383

FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-50

Query Match 98.6%; Score 1378; DB 3; Length 273;
Best Local Similarity 98.5%; Pred. No. 2,5e-132;
Matches 269; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKTQWITLCIYLLFNPVLTGEGICRNFVNNVQVTKLVANLPKQWITLKYYVG 60
DB 1 MKKTQWITLCIYLLFNPVLTGEGICRNFVNNVQVTKLVANLPKQWITLKYYVG 60
QY 61 MDVLSHCISMVYVQVLSLTDLLDKFENISEGLSNYSIIDKLVNIYVDLVCEKENS 120
DB 61 MDVLSHCISMVYVQVLSLTDLLDKFENISEGLSNYSIIDKLVNIYVDLVCEKENS 120
QY 121 KDLKSPKSPERLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVST 180
DB 121 KDLKSPKSPERLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVST 180
QY 181 KPFMLPVAASSLRNDSSSNRKAQNPQDSSLHMAAMALPALFSLIIGFAGALYMKR 240
DB 181 KPFMLPVAASSLRNDSSSNRKAQNPQDSSLHMAAMALPALFSLIIGFAGALYMKR 240
QY 241 QPSLTRAVENTIOINEDNEISMLQEKERFQEV 273
DB 241 QPSLTRAVENTIOINEDNEISMLQEKERFQEV 273

RESULT 15
US-08-955-848A-82
Sequence 82, Application US/08955848A
Patent No. 5969105
GENERAL INFORMATION:
APPLICANT: Mc Whorter, Charles
TITLE OF INVENTION: No. 5969105el Stem Cell Factor Receptor
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: G. D. Searle & Co.
STREET: P. O. Box 5110
CITY: Chicago
STATE: IL
COUNTRY: U. S. A.
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,848A
FILING DATE: 21-OCT-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,165
FILING DATE: 25-OCT-1997
ATTORNEY/AGENT INFORMATION:

NAME: Bennett, Dennis A
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2992/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-737-6986
TELEFAX: 314-737-6972
TELEX:
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-955-848A-82

Query Match 90.6%; Score 1265; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 7.1e-121;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 EGICRNRVTNNVQVTKLVANLPKQWITLKYYVQGMVLPSSHCMISEMVOVLSLTDLL 85
DB 1 EGICRNRVTNNVQVTKLVANLPKQWITLKYYVQGMVLPSSHCMISEMVOVLSLTDLL 85
QY 86 DKFSNISEGLSNYSIIDKLVNIYVDLVCEKENSCKDLKSPKSPERLFTPEEFRIEN 145
DB 61 DKFSNISEGLSNYSIIDKLVNIYVDLVCEKENSCKDLKSPKSPERLFTPEEFRIEN 120
QY 146 RSIDAFKDFVASETSDCVSSTLSPKDSRVSTYTKPFMLPVAASSLRNDSSSNRKA 205
DB 121 RSIDAFKDFVASETSDCVSSTLSPKDSRVSTYTKPFMLPVAASSLRNDSSSNRKA 180
QY 206 NPPGDSLHMAAMALPALFSLIIGFAGALYMKRQPSLTRAVENTIOINEDNEISMLQ 265
DB 181 NPPGDSLHMAAMALPALFSLIIGFAGALYMKRQPSLTRAVENTIOINEDNEISMLQ 240
QY 266 KEREFQEV 273
DB 241 KEREFQEV 248

Search completed: February 5, 2004, 15:12:23
Job time : 15.2893 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 15:07:35 ; Search time 30.4587 Seconds
(without alignments)
1876.686 Million cell updates/sec

Title: US-09-224-683-61

Perfect score: 1397
Sequence: 1 MKKTQWILITCIYQLLEFN.....NEEDNEISMLQEKERFQEV 273

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications_AA*

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2: /cgn2_6/ptodata/2/pubppaa/PCR_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1397	100.0	273	9 US-09-005-243-49	Sequence 49, Appl
2	1397	100.0	273	9 US-09-005-243-61	Sequence 61, Appl
3	1397	100.0	273	9 US-09-224-683-49	Sequence 49, Appl
4	1397	100.0	273	9 US-09-224-683-61	Sequence 61, Appl
5	1392	99.6	273	9 US-09-005-243-48	Sequence 48, Appl
6	1392	99.6	273	9 US-09-224-683-48	Sequence 48, Appl
7	1381	98.9	273	9 US-09-005-243-50	Sequence 50, Appl
8	1381	98.9	273	9 US-09-224-683-50	Sequence 50, Appl
9	1332.5	88.2	266	9 US-09-005-243-57	Sequence 57, Appl
10	1332.5	88.2	266	9 US-09-224-683-57	Sequence 57, Appl
11	1231	88.1	245	9 US-09-005-243-63	Sequence 63, Appl
12	1231	88.1	245	9 US-09-224-683-63	Sequence 63, Appl
13	1180.5	84.5	274	9 US-09-005-243-51	Sequence 51, Appl
14	1180.5	84.5	274	9 US-09-224-683-51	Sequence 51, Appl
15	1179.5	84.4	271	9 US-09-005-243-52	Sequence 52, Appl

16	1179.5	84.4	271	9	US-09-224-683-52
17	1173	84.0	273	9	US-09-005-243-53
18	1173	84.0	273	9	US-09-224-683-53
19	1158	82.9	273	9	US-09-005-243-42
20	1158	82.9	273	9	US-09-224-683-42
21	1157	82.8	273	9	US-09-005-243-55
22	1157	82.8	273	9	US-09-224-683-55
23	1157	82.8	273	15	US-10-132-243-54
24	1151	82.4	273	9	US-09-005-243-54
25	1151	82.4	273	9	US-09-224-683-54
26	1066	76.3	270	15	US-10-132-243-52
27	1030	73.7	208	9	US-09-005-243-46
28	1030	73.7	208	9	US-09-224-683-46
29	865	61.9	195	9	US-09-005-243-44
30	865	61.9	195	9	US-09-224-683-44
31	843	60.3	166	9	US-09-748-592-2
32	839	60.1	164	10	US-09-903-3272-10
33	839	60.1	165	12	US-10-320-231A-25
34	839	60.1	165	15	US-10-053-355A-2
35	839	60.1	393	15	US-10-270-555-1
36	837	59.9	613	10	US-09-903-3272-14
37	826	59.1	196	9	US-09-005-243-40
38	826	59.1	196	9	US-09-224-683-40
39	683	48.9	282	9	US-09-005-243-56
40	683	48.9	282	9	US-09-224-683-56
41	679	48.6	165	9	US-09-005-243-1
42	679	48.6	165	9	US-09-224-683-1
43	667	47.7	393	15	US-10-270-555-2
44	315	22.5	82	9	US-09-005-243-59
45	315	22.5	82	9	US-09-224-683-59

ALIGNMENTS

RESULT 1
US-09-005-243-49
; Sequence 49, Application US/09005243
; Patent No. US20020018763A1
; GENERAL INFORMATION:
; APPLICANT: Zeebo, Kristina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borum
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,243
; FILING DATE:
; CLASSIFICATION:
; APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:

Sequence 52, Appl
Sequence 53, Appl
Sequence 54, Appl
Sequence 42, Appl
Sequence 44, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 2, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 44, Appl
Sequence 14, Appl
Sequence 2, Appl
Sequence 10, Appl
Sequence 25, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 40, Appl
Sequence 40, Appl
Sequence 56, Appl
Sequence 56, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 59, Appl
Sequence 59, Appl

APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA: 07/537,198
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-49

Query Match 100.0%; Score 1397; DB 9; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.8e-127;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLFPNPLVTEGICRNRVTNNVADVTKLVANLPKDYMITLKVPV 60
DB 1 MKKTQWTLTCTIYQLLFPNPLVTEGICRNRVTNNVADVTKLVANLPKDYMITLKVPV 60
QY 61 MDVLPSCWISSEMVVQSDSLTDLDFKSNISEGLSNYSIIDKLVNIVDLVECKENSS 120
DB 61 MDVLPSCWISSEMVVQSDSLTDLDFKSNISEGLSNYSIIDKLVNIVDLVECKENSS 120
QY 121 KDLKSKFKSPPEPLFTPEEPFRIFNRSIDAFKDFVVASSETSDCVSSSTLSPEKDSRVSVT 180
DB 121 KDLKSKFKSPPEPLFTPEEPFRIFNRSIDAFKDFVVASSETSDCVSSSTLSPEKDSRVSVT 180
QY 181 KPEMLPVAASSLRNDSSSNRKAKNPGDSSLHMAAMALPALPSLIIGFAGALYMKR 240
DB 181 KPEMLPVAASSLRNDSSSNRKAKNPGDSSLHMAAMALPALPSLIIGFAGALYMKR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 2

US-09-005-243-61
Sequence 61, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-61

Query Match 100.0%; Score 1397; DB 9; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.8e-127;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLFPNPLVTEGICRNRVTNNVADVTKLVANLPKDYMITLKVPV 60
DB 1 MKKTQWTLTCTIYQLLFPNPLVTEGICRNRVTNNVADVTKLVANLPKDYMITLKVPV 60
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DB 61 MDVLPSCWISSEMVVQSDSLTDLDFKSNISEGLSNYSIIDKLVNIVDLVECKENSS 120
QY 121 KDLKSKFKSPPEPLFTPEEPFRIFNRSIDAFKDFVVASSETSDCVSSSTLSPEKDSRVSVT 180
DB 121 KDLKSKFKSPPEPLFTPEEPFRIFNRSIDAFKDFVVASSETSDCVSSSTLSPEKDSRVSVT 180
QY 181 KPEMLPVAASSLRNDSSSNRKAKNPGDSSLHMAAMALPALPSLIIGFAGALYMKR 240
DB 181 KPEMLPVAASSLRNDSSSNRKAKNPGDSSLHMAAMALPALPSLIIGFAGALYMKR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 3

US-09-224-683-49
Sequence 49, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-49

Query Match 100.0%; Score 1397; DB 9; Length 273;
Best Local Similarity 100.0%; Pred. No. 1,8e-127;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFPLVKTGICNRRTNNKYDTKIVANLPKRYMTTLTKVPG 60
DB 1 MKKTQWILTCIYQLLEFPLVKTGICNRRTNNKYDTKIVANLPKRYMTTLTKVPG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDDKFSNISSEGLSYSTIIDKLVNVDLVCVENSS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDDKFSNISSEGLSYSTIIDKLVNVDLVCVENSS 120
QY 121 KDLKSKSPSPRLFTPEEFRRIFNRSIDAFCQVVASETSDCVSSSTLSPKDSRVSVT 180
DB 121 KDLKSKSPSPRLFTPEEFRRIFNRSIDAFCQVVASETSDCVSSSTLSPKDSRVSVT 180

QY 181 KPFLPVAASLRNDSSSNRKAKNPPGDSLLHMAAMALPALPSLIIGFAGALYMKR 240
DB 181 KPFLPVAASLRNDSSSNRKAKNPPGDSLLHMAAMALPALPSLIIGFAGALYMKR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLQEKEREPOEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLQEKEREPOEV 273

RESULT 4
US-09-224-683-61
Sequence 61, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suges, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-224-683-61

Query Match 100.0%; Score 1397; DB 9; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.8e-127;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLEFNPVLTGICNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
DB 1 MKKTQWTLTCTIYQLLEFNPVLTGICNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
QY 61 MDVLPSCWISSENVQVLSLTDLLDKFSNISGLSNYSIIDKLVNIYVDLVCEKENS 120
DB 61 MDVLPSCWISSENVQVLSLTDLLDKFSNISGLSNYSIIDKLVNIYVDLVCEKENS 120
QY 121 KDLKKSFKSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
DB 121 KDLKKSFKSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
QY 181 KPFLPVAASSLRNDSSSNRKAKNPPGDSLSHMAALPALFSLIIGFAGALYMKR 240
DB 181 KPFLPVAASSLRNDSSSNRKAKNPPGDSLSHMAALPALFSLIIGFAGALYMKR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 5
US-09-005-243-48
Sequence 48, Application US/09005243
Patent No. US20020018763A1

GENERAL INFORMATION:

APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383

FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-48

Query Match 99.6%; Score 1392; DB 9; Length 273;
Best Local Similarity 99.6%; Pred. No. 5.6e-127;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLEFNPVLTGICNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
DB 1 MKKTQWTLTCTIYQLLEFNPVLTGICNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
QY 61 MDVLPSCWISSENVQVLSLTDLLDKFSNISGLSNYSIIDKLVNIYVDLVCEKENS 120
DB 61 MDVLPSCWISSENVQVLSLTDLLDKFSNISGLSNYSIIDKLVNIYVDLVCEKENS 120
QY 121 KDLKKSFKSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
DB 121 KDLKKSFKSPPEPRLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
QY 181 KPFLPVAASSLRNDSSSNRKAKNPPGDSLSHMAALPALFSLIIGFAGALYMKR 240
DB 181 KPFLPVAASSLRNDSSSNRKAKNPPGDSLSHMAALPALFSLIIGFAGALYMKR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 6
US-09-224-683-48

Sequence 48, Application US/09224683
Patent No. US2002001491A1

GENERAL INFORMATION:

APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-48

Query Match 99.6%; Score 1392; DB 9; Length 273;
Best Local Similarity 99.6%; Pred. No. 5.6e-127;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWMLTCTYLLQLLFNPLVKTGICRNRTNNVQDTLVANLPKDYMITLKYVG 60
DB 1 MKKTQWMLTCTYLLQLLFNPLVKTGICRNRTNNVQDTLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISSEMVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
DB 61 MDVLPSCWISSEMVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
QY 121 KDLKSKFSKPEPRLTPTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSYT 180
DB 121 KDLKSKFSKPEPRLTPTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSYT 180
QY 181 KPMLPVAASSLRNDSSSNRKAKNPPGDSLSLHMAAMLPALFSLITGFAFGALYWKRR 240
DB 181 KPMLPVAASSLRNDSSSNRKAKNPPGDSLSLHMAAMLPALFSLITGFAFGALYWKRR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLQEKERFQEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLQEKERFQEV 273

RESULT 7
US-09-005-243-50
Sequence 50, Application US/09005243
Patent No. US2002018763A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Boseelman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-50

Query Match 98.9%; Score 1381; DB 9; Length 273;
Best Local Similarity 98.9%; Pred. No. 6.5e-126;
Matches 270; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKTQWMLTCTYLLQLLFNPLVKTGICRNRTNNVQDTLVANLPKDYMITLKYVG 60
DB 1 MKKTQWMLTCTYLLQLLFNPLVKTGICRNRTNNVQDTLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISSEMVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
DB 61 MDVLPSCWISSEMVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
QY 121 KDLKSKFSKPEPRLTPTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSYT 180
DB 121 KDLKSKFSKPEPRLTPTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKDSRVSYT 180
QY 181 KPMLPVAASSLRNDSSSNRKAKNPPGDSLSLHMAAMLPALFSLITGFAFGALYWKRR 240
DB 181 KPMLPVAASSLRNDSSSNRKAKNPPGDSLSLHMAAMLPALFSLITGFAFGALYWKRR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLQEKERFQEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLQEKERFQEV 273

RESULT 8

US-09-224-683-50
Sequence 50, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-50

Query Match 98.9%; Score 1381; DB 9; Length 273;
Best Local Similarity 98.9%; Pred. No. 6.5e-126;
Matches 270; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVKTGICRRNVTNNVADVTQLVANLPKDYMTLLKYYVG 60
DB 1 MKKTQWILTCIYQLLEFNPVKTGICRRNVTNNVADVTQLVANLPKDYMTLLKYYVG 60
QY 61 MOVLPSCWISNMVQVLSLTDLLDKFSNISEGINSYIIDKLVNIYDDLVECKENSS 120
DB 61 MOVLPSCWISNMVQVLSLTDLLDKFSNISEGINSYIIDKLVNIYDDLVECKENSS 120
QY 121 KOLKSPKSPERPLTPPEFPFRIFNRSIDAFKDFVAVASSETSDCVSSTLSPKDSRVSVT 180
DB 121 KOLKSPKSPERPLTPPEFPFRIFNRSIDAFKDFVAVASSETSDCVSSTLSPKDSRVSVT 180
QY 181 KFMPLPYVASSLRNDSSSNRKAKNPPGDSLHWAMALPALFSLIIGFAFALYMKR 240
DB 181 KFMPLPYVASSLRNDSSSNRKAKNPPGDSLHWAMALPALFSLIIGFAFALYMKR 240
QY 241 QPSLTRAVENTIOINEDNEISMLCKEKEFEQEV 273
DB 241 QPSLTRAVENTIOINEDNEISMLCKEKEFEQEV 273

RESULT 9

US-09-005-243-57
Sequence 57, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 266 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-005-243-57

Query Match 88.2%; Score 1232.5; DB 9; Length 266;
 Best Local Similarity 91.9%; Pred. No. 1.7e-111;
 Matches 251; Conservative 9; Mismatches 6; Indels 7; Gaps 5;

QY 1 MKKTQWMLITCIYQLLHFNPLVKTGICRNRTVNVKDTKLVANLPKDYMITLKYVG 60
 DB 1 MKKTQWMLITCIYQLLHFNPLVKT-GICRNRTV-DVKDTKLVANLPKDYMITLKYVG 58
 QY 61 MDVLPSCWISSEWVQSLDLDLDFKSNISSEGLSNYSIIDKLVIIVDDLVCEKENS 120
 DB 59 MDVLPSCWISSEWVQSLDLDLDFKSNISSEGLSNYSIIDKLVIIVDDLVCEC-EENSS 117
 QY 121 KDLKSKFSPRLFTPEEFRIENRSIDAFKDFVASETSDCVSSTLSPKDSRVSVT 180
 DB 118 KDVKKS-KSPRLFTPEEFRIENRSIDAFKDFVASETSDCVSSTLSPKDSRVSVT 176
 QY 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSLSHMAAMLPALFSLIIGAFGALYMKR 240
 DB 177 KPFMLPVAASSLRNDSSSNRKANE---DSSLQMAAMLPALFSLIIGAFGALYMKR 233
 QY 241 QPSLTRAVENTIOINEEDNEISMLQEKERFQEV 273
 DB 234 QPSLTRAVENTIOINEEDNEISMLQEKERFQEV 266

RESULT 10
 US-09-224-683-57

Sequence 57, Application US/09224683
 Patent No. US20020031491A1
 GENERAL INFORMATION:
 APPLICANT: Zeebo, Kristina M.
 APPLICANT: Boeselman, Robert A.
 APPLICANT: Suggs, Sidney V.
 APPLICANT: Martin, Francis H.
 TITLE OF INVENTION: Stem Cell Factor: Composition Claims
 NUMBER OF SEQUENCES: 104
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/224,683
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/005,893
 FILING DATE: 12-JAN-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/449,653
 FILING DATE: 24-MAY-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/982,255

FILING DATE: 25-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/589,701
 FILING DATE: 01-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/573,616
 FILING DATE: 24-AUG-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/537,198
 FILING DATE: 11-JUN-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/422,383
 FILING DATE: 16-OCT-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Clough, David W.
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET NUMBER: 01017/35136
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEFAX: 312/474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 266 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-224-683-57

Query Match 88.2%; Score 1232.5; DB 9; Length 266;
 Best Local Similarity 91.9%; Pred. No. 1.7e-111;
 Matches 251; Conservative 9; Mismatches 6; Indels 7; Gaps 5;

QY 1 MKKTQWMLITCIYQLLHFNPLVKTGICRNRTVNVKDTKLVANLPKDYMITLKYVG 60
 DB 1 MKKTQWMLITCIYQLLHFNPLVKT-GICRNRTV-DVKDTKLVANLPKDYMITLKYVG 58
 QY 61 MDVLPSCWISSEWVQSLDLDLDFKSNISSEGLSNYSIIDKLVIIVDDLVCEKENS 120
 DB 59 MDVLPSCWISSEWVQSLDLDLDFKSNISSEGLSNYSIIDKLVIIVDDLVCEC-EENSS 117
 QY 121 KDLKSKFSPRLFTPEEFRIENRSIDAFKDFVASETSDCVSSTLSPKDSRVSVT 180
 DB 118 KDVKKS-KSPRLFTPEEFRIENRSIDAFKDFVASETSDCVSSTLSPKDSRVSVT 176
 QY 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSLSHMAAMLPALFSLIIGAFGALYMKR 240
 DB 177 KPFMLPVAASSLRNDSSSNRKANE---DSSLQMAAMLPALFSLIIGAFGALYMKR 233
 QY 241 QPSLTRAVENTIOINEEDNEISMLQEKERFQEV 273
 DB 234 QPSLTRAVENTIOINEEDNEISMLQEKERFQEV 266

RESULT 11
 US-09-005-243-63

Sequence 63, Application US/09005243
 Patent No. US20020018763A1
 GENERAL INFORMATION:
 APPLICANT: Zeebo, Kristina M.
 APPLICANT: Boeselman, Robert A.
 APPLICANT: Suggs, Sidney V.
 APPLICANT: Martin, Francis H.
 TITLE OF INVENTION: Stem Cell Factor
 NUMBER OF SEQUENCES: 104
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-63

Query Match 88.1%; Score 1231; DB 9; Length 245;
Best Local Similarity 89.4%; Pred. No. 2.2e-111;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWTLTCTIYQLLEFNPVLTBEGICRNRVTNNVQVTKLVANLPRDYMITLKYPG 60
DB 1 MKKTQWTLTCTIYQLLEFNPVLTBEGICRNRVTNNVQVTKLVANLPRDYMITLKYPG 60
QY 61 MDVLPBHCWISSEWVQVSDSLTDLDDKFSNISSEGLSNYSIIDKLVINIVDDIVECVKENS 120
DB 61 MDVLPBHCWISSEWVQVSDSLTDLDDKFSNISSEGLSNYSIIDKLVINIVDDIVECVKENS 120
QY 121 KDLKSFKSPBPLFTPEEFPRIFNRSIDAFKDFVAVASTQCVVSTISPEKDSRVST 180
DB 121 KDLKSFKSPBPLFTPEEFPRIFNRSIDAFKDFVAVASTQCVVSTISPEKDSRVST 180
QY 121 KDLKSFKSPBPLFTPEEFPRIFNRSIDAFKDFVAVASTQCVVSTISPEKDSRVST 174
DB 121 KDLKSFKSPBPLFTPEEFPRIFNRSIDAFKDFVAVASTQCVVSTISPEKDSRVST 174
QY 181 KPFMLPPVAASSLRNDSSSNRKAQNPQDSSSLHMAAALPALFSLIIFAFGALYWKRR 240
DB 175 -----KAKNPQDSSSLHMAAALPALFSLIIFAFGALYWKRR 212
QY 241 QPSLTRAVERNIOINEDNEISMIOEKERPEOEY 273
DB 213 QPSLTRAVERNIOINEDNEISMIOEKERPEOEY 245

RESULT 12
US-09-224-683-63
Sequence 63, Application US/09224683
Patent No. US20020031491A1

GENERAL INFORMATION:
APPLICANT: Zeebo, Kriesztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-63

Query Match 88.1%; Score 1231; DB 9; Length 245;
Best Local Similarity 89.4%; Pred. No. 2.2e-111;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWTLTCTIYQLLEFNPVLTBEGICRNRVTNNVQVTKLVANLPRDYMITLKYPG 60
DB 1 MKKTQWTLTCTIYQLLEFNPVLTBEGICRNRVTNNVQVTKLVANLPRDYMITLKYPG 60
QY 61 MDVLPBHCWISSEWVQVSDSLTDLDDKFSNISSEGLSNYSIIDKLVINIVDDIVECVKENS 120
DB 61 MDVLPBHCWISSEWVQVSDSLTDLDDKFSNISSEGLSNYSIIDKLVINIVDDIVECVKENS 120

QY 121 KDLKSKFKSPPEPLFTPEEFRIIENRSDAFKDFVAVASSTSCVVSSTLSPEKDSRVSVT 180
DB 121 KDLKSKFKSPPEPLFTPEEFRIIENRSDAFKDFVAVASSTSCVVSSTLSPEK----- 174
QY 181 KPFMLPVAASSLRNDSSSNRKAKPPGDSLSHMAALPALFSLIIGFAGALYWK 240
DB 175 -----KAKNPBGDSLSHMAALPALFSLIIGFAGALYWK 212
QY 241 OPSLTRAVENTIOINEEDNEISMLOEKEREOEV 273
DB 213 OPSLTRAVENTIOINEEDNEISMLOEKEREOEV 245
RESULT 13
US-09-005-243-51
Sequence 51, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Boeselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO.: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-51
Query Match 84.5%; Score 1180.5; DB 9; Length 274;
Best Local Similarity 85.4%; Pred. No. 2.1e-106;
Matches 234; Conservative 17; Mismatches 22; Indels 1; Gaps 1;
QY 1 MKKTQTWLTCTIYQLLFNPLVKTGICRRRVNINNVQVTKLVANLPKDYMITLTKYVG 60
DB 1 MKKTQTWLTCTIYQLLFNPLVKTGICRRRVNINNVQVTKLVANLPKDYMITLTKYVG 60
QY 61 MDVLPSSHCMISBMVQSLDLDLDRKSNISEGLSNYSIDKLVNIVDVLVECKENSS 120
DB 61 MDVLPSSHCMISBMVQSLDLDLDRKSNISEGLSNYSIDKLVNIVDVLVECKENSS 120
QY 121 KDLKSKFKSPPEPLFTPEEFRIIENRSDAFKDFVAVASSTSCVVSSTLSPEKDSRVSV 179
DB 121 ENVKAPKSPPEPLFTPEEFRIIENRSDAFKDFVAVASSTSCVVSSTLSPEKDSRVSV 180
QY 180 TKPFMLPVAASSLRNDSSSNRKAKPPGDSLSHMAALPALFSLIIGFAGALYWK 239
DB 181 TKPFMLPVAASSLRNDSSSNRKAKPPGDSLSHMAALPALFSLIIGFAGALYWK 240
QY 240 RQPSLTRAVENTIOINEEDNEISMLOEKEREOEV 273
DB 241 RQPSLTRAVENTIOINEEDNEISMLOEKEREOEV 274
RESULT 14
US-09-224-683-51
Sequence 51, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Boeselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-51

Query Match      84.5%; Score 1180.5; DB 9; Length 274;
Best Local Similarity 85.4%; Pred. No. 2.1e-106;
Matches 234; Conservative 17; Mismatches 22; Indels 1; Gaps 1;

QY 1 MKKTQWILTCIYLQLLFNPVLVKTGICRNRYTNVVKDVKLVANLPKDYMTLLKVVVG 60
DB 1 MKKTQWILTCIYLQLLFNPVLVKTGICRNRYTNVVKDVKLVANLPKDYMTLLKVVVG 60
QY 61 MDVLPSCWISWVVOVLSLTDLDKFSNISGLSNYSIIDLVNIIVDDLVCEVKNSSKD 120
DB 61 MDVLPSCWISWVVOVLSLTDLDKFSNISGLSNYSIIDLVNIIVDDLVCEVKNSSKD 120
QY 61 MDVLPSCWISWVVOVLSLTDLDKFSNISGLSNYSIIDLVNIIVDDLVCEVKNSSKD 120
DB 61 MDVLPSCWISWVVOVLSLTDLDKFSNISGLSNYSIIDLVNIIVDDLVCEVKNSSKD 120
QY 121 KDIKSKSPKPEPLFTPEEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPKDSRVSV 179
DB 121 KDIKSKSPKPEPLFTPEEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPKDSRVSV 179
QY 121 ENVKKAPKSPBELFTPEEFRIFNRSIDAFKDLFTVASKSPSCVVSSTLSPKDSRVSV 180
DB 121 ENVKKAPKSPBELFTPEEFRIFNRSIDAFKDLFTVASKSPSCVVSSTLSPKDSRVSV 180
QY 180 TPEFMLPVAASLRLNDSSSNRKAKNPQDSSIHMAAMALPFLSLIIGFAFGALYWKX 239
DB 181 TPEFMLPVAASLRLNDSSSNRKAKNSIGDSMLQAAVALPFAFSLVIGFAGALYWKX 240
QY 240 RPSLTRAVENTIOINEEDNEISMLOEKEREFOEV 273
DB 241 KQPNLRTVENIOINEEDNEISMLOEKEREFOEV 274

RESULT 15
US-09-005-243-52
Sequence 52, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristzina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-52

Query Match      84.4%; Score 1179.5; DB 9; Length 271;
Best Local Similarity 86.4%; Pred. No. 2.5e-106;
Matches 235; Conservative 17; Mismatches 17; Indels 3; Gaps 3;

QY 3 KTQFWILTCIYLQLLFNPVLVKTGICRNRYTNVVKDVKLVANLPKDYMTLLKVVPM 62
DB 2 KTQFWILTCIYLQLLFNPVLVKTGICRNRYTNVVKDVKLVANLPKDYMTLLKVVPM 60
QY 63 VLPSHCWISWVVOVLSLTDLDKFSNISGLSNYSIIDLVNIIVDDLVCEVKNSSKD 122
DB 61 VLPSHCWISWVVOVLSLTDLDKFSNISGLSNYSIIDLVNIIVDDLVCEVKNSSKD 120
QY 123 LKSKSPKPEPLFTPEEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPKDSRVSVTK 181
DB 121 VKSKSPKPEPLFTPEEFRIFNRSIDAFKDLFTVASKSPSCVVSSTLSPKDSRVSVTK 180
QY 182 PFMPLPVAASLRLNDSSSNRKAKNPQDSSIHMAAMALPFLSLIIGFAFGALYWKXQ 241
DB 181 PFMPLPVAASLRLNDSSSNRKAT-NPIEDSSIQAAVALPFAFSLVIGFAGALYWKXQ 239
QY 242 PSLTRAVENTIOINEEDNEISMLOEKEREFOEV 273
DB 240 PNLRTVENIOINEEDNEISMLOEKEREFOEV 271

Search completed: February 5, 2004, 15:23:27
Job time : 31.4587 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 15:00:43 ; Search time 15.4174 Seconds
(without alignments)
1702.889 Million cell updates/sec

Title: US-09-224-683-61

Perfect score: 1397
Sequence: 1 MKKTQWILTCIYLQLLFN.....NEEDNEISMLQEKERFQEV 273

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1397	100.0	273	2 A35974	mast cell growth f
2	1231	88.1	245	2 B61190	mast cell growth f
3	1203.5	86.1	274	2 I46575	c-kit ligand - pig
4	1184.5	84.8	274	2 S47571	stem cell factor,
5	1180.5	84.5	274	2 I46929	stem cell factor -
6	1157	82.8	273	2 S65801	mast cell growth f
7	991	70.9	245	2 A37934	mast cell growth f
8	885.5	63.4	202	2 S58313	stem cell factor p
9	857	61.3	201	2 B35974	stem cell factor p
10	703	50.3	287	2 JN0637	stem cell factor p
11	702	50.3	287	2 S70366	stem cell factor p
12	589	42.2	253	2 S70367	stem cell factor 1
13	576.5	41.3	124	2 S29052	stem cell factor s
14	175.5	12.6	51	2 B35971	mast cell growth f
15	172.5	12.3	49	2 A35971	mast cell growth f
16	106	7.6	465	2 H97165	flagellar hook-len
17	101	7.2	1490	2 T16086	hypothetical prote
18	100.5	7.2	402	2 T09062	probable advanced
19	100.5	7.2	647	2 F90585	conserved hypothet
20	97.5	7.0	1107	2 S61687	probable membrane
21	97	6.9	1447	2 F82909	hypothetical prote
22	95.5	6.8	484	2 T25944	hypothetical prote
23	95.5	6.7	614	2 B86461	hypothetical prote
24	93.5	6.7	1293	2 T27886	hypothetical prote
25	93.5	6.7	1813	2 T19295	hypothetical prote
26	92.5	6.6	164	2 B69616	cell-division init
27	92.5	6.6	246	2 T19850	hypothetical prote
28	92.5	6.6	398	2 I53340	paired box transcr
29	92.5	6.6	512	2 G86773	citrate (pro-3s)-1

30	91.5	6.5	575	2 D84668	hypothetical prote
31	91.5	6.5	767	2 T19690	hypothetical prote
32	90.5	6.5	251	2 B86647	hypothetical prote
33	90.5	6.5	616	2 A69136	ATP-dependent Clp
34	90.5	6.5	1425	2 E89303	protein C47E8.8 fi
35	90.5	6.5	1675	2 T31473	hypothetical prote
36	90	6.4	378	2 F64300	formate dehydrogen
37	90	6.4	774	2 T32987	hypothetical prote
38	90	6.4	2100	2 T38128	c7123.15 protein -
39	89.5	6.4	268	2 G81257	probable hemain up
40	89.5	6.4	335	2 S44922	K18 antigen - Entra
41	89.5	6.4	384	2 H64161	hypothetical prote
42	89	6.4	242	2 T27226	hypothetical prote
43	89	6.4	292	2 B71733	hypothetical prote
44	89	6.4	982	2 T15967	hypothetical prote
45	88.5	6.3	378	2 T25672	hypothetical prote

ALIGNMENTS

RESULT 1

A35974
mast cell growth factor precursor - human
N:Alternate names: Kit ligand; stem cell factor
C:Species: Homo sapiens (man)
C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C/Accession: A35974; A61190
S:Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.J.
S; J.C.; Patel, A.C.; Fisher, E.F.; Erjavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev, I
Cell 63, 203-211, 1990
A>Title: Primary structure and functional expression of rat and human stem cell factor 1
A:Reference number: A35974; MUID:91004219; PMID:12208279
A:Accession: A35974
A:Molecule type: mRNA
A:Residues: 1-273 <MAR>
A:Cross-references: GB:M59964; NID:G37933; PIDN:AAA85450.1; PID:G37934
R:Anderson, D.M.; Williams, D.E.; Tushnets, R.; Gimpel, S.; Eisenman, J.; Cannizzaro, J
Cell Growth Differ. 2, 373-378, 1991
A>Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localiz
A:Reference number: A61190; MUID:92172791; PMID:1724381
A:Accession: A61190
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-273 <AND>
C:Genetics: GDB:MGF
A:Gene: GDB:MGF
A:Cross-references: GDB:128026; OMIM:184745
A:Map position: 12q22-12q22
C:Superfamily: mouse mast cell growth factor
C:Keywords: alternative splicing; extracellular protein; glycoprotein; transmembrane pro
F;1-25/Domain: signal sequence #status predicted <Sig>
F;26-273/Product: mast cell growth factor #status predicted <MCS>
F;26-189/Product: (or 26-190) mast cell growth factor, soluble form #status predicted <r
F;215-237/Domain: transmembrane #status predicted <TM>
F;90,97,118,145,195/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 100.0%; Score 1397; DB 2; Length 273;

Best Local Similarity 100.0%; Pred. No. 6.6e-103;

Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKKTQWILTCIYLQLLFNPLVKTGICRNVTNNVQVTLVNLKPDVMTTKYVPG	60
DB	1	MKKTQWILTCIYLQLLFNPLVKTGICRNVTNNVQVTLVNLKPDVMTTKYVPG	60
QY	61	MDVLSHCWISSEMVQSLTDLDDKFSNISSEGLSNYSIIDKLNVIVDDLVCEVENS	120
DB	61	MDVLSHCWISSEMVQSLTDLDDKFSNISSEGLSNYSIIDKLNVIVDDLVCEVENS	120
QY	121	KDLKSFSPSPRLTPEEFRIINRSIDAFQPVVASTSCVVSSTLSPKDSRVST	180
DB	121	KDLKSFSPSPRLTPEEFRIINRSIDAFQPVVASTSCVVSSTLSPKDSRVST	180

QY 181 KPMP.LPVAASSLRNDSSSNRKAKNPGDSSLHMAAMALPALFSLIIGFAGALYWKX 240
 Db 181 KPMP.LPVAASSLRNDSSSNRKAKNPGDSSLHMAAMALPALFSLIIGFAGALYWKX 240
 QY 241 QPSTLRAVENIQINEEDNEISMLQEKEREFQEV 273
 Db 241 QPSTLRAVENIQINEEDNEISMLQEKEREFQEV 273

RESULT 2

B61190
 mast cell growth factor, short form precursor - human
 N:Alternate names: Kit ligand, short form; stem cell factor, short form
 C:Species: Homo sapiens (man)
 C:Date: 03-May-1994 #sequence_rev1sion 03-May-1994 #text_change 21-Jul-2000
 C:Accession: B61190
 R:Anderson, D.M.; Williams, D.E.; Tushinski, R.; Gimpel, S.; Eisenman, J.; Camizazzo, L.
 Cell Growth Differ. 2, 373-378, 1991
 A:Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localiza
 A:Reference number: A61190; MID:92172791; PMID:1724381
 A:Accession: B61190
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-245 <AND>
 C:Comment: Alternative splicing produces this short form in which a predicted cleavage s
 C:Gene: GDB:MGF
 A:Cross-references: GDB:128026; OMIM:184745
 A:Map position: 12q22-12q22
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: alternative splicing; glycoprotein; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:187-209/Domain: transmembrane #status predicted <TMN>
 F:90, 97, 118, 145/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.1%; Score 1231; DB 2; Length 245;
 Best Local Similarity 89.4%; Pred. No. 7, 3e-90;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWTLITCTIYQLLEFPLVKTGICRRRTVNNVQVTKLVANLPKDYMITLKYPVG 60
 Db 1 MKKTQWTLITCTIYQLLEFPLVKTGICRRRTVNNVQVTKLVANLPKDYMITLKYPVG 60
 QY 61 MDVLPSCWISSEWVQSLDLDLDFKSNISEGLSNYSIIDKLVIIVDDIVECVKENS 120
 Db 61 MDVLPSCWISSEWVQSLDLDLDFKSNISEGLSNYSIIDKLVIIVDDIVECVKENS 120
 QY 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSV 180
 Db 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSV 174
 QY 181 KPMP.LPVAASSLRNDSSSNRKAKNPGDSSLHMAAMALPALFSLIIGFAGALYWKX 240
 Db 181 KPMP.LPVAASSLRNDSSSNRKAKNPGDSSLHMAAMALPALFSLIIGFAGALYWKX 212
 QY 241 QPSTLRAVENIQINEEDNEISMLQEKEREFQEV 273
 Db 241 QPSTLRAVENIQINEEDNEISMLQEKEREFQEV 245

RESULT 3

146575
 c-kit ligand - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_rev1sion 21-Feb-1997 #text_change 21-Jul-2000
 C:Accession: 146575
 R:Zhang, Z.; Anthony, R.V.
 Biol. Reprod. 50, 95-102, 1994
 A:Title: Porcine stem cell factor/c-kit ligand: its molecular cloning and localization
 A:Reference number: 146575; MID:94146218; PMID:7508758
 A:Accession: 146575
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA

A:Residues: 1-274 <ZHA>
 A:Cross-references: GB:L07786; NID:9164420; PIDN:AAA53670.1; PID:9164421
 C:Superfamily: mouse mast cell growth factor

Query Match 86.1%; Score 1203.5; DB 2; Length 274;
 Best Local Similarity 85.8%; Pred. No. 1, 3e-87;
 Matches 235; Conservative 22; Mismatches 16; Indels 1; Gaps 1;

QY 1 MKKTQWTLITCTIYQLLEFPLVKTGICRRRTVNNVQVTKLVANLPKDYMITLKYPVG 60
 Db 1 MKKTQWTLITCTIYQLLEFPLVKTGICRRRTVNNVQVTKLVANLPKDYMITLKYPVG 60
 QY 61 MDVLPSCWISSEWVQSLDLDLDFKSNISEGLSNYSIIDKLVIIVDDIVECVKENS 120
 Db 61 MDVLPSCWISSEWVQSLDLDLDFKSNISEGLSNYSIIDKLVIIVDDIVECVKENS 120
 QY 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSV 179
 Db 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSV 180
 QY 180 TKPMP.LPVAASSLRNDSSSNRKAKNPGDSSLHMAAMALPALFSLIIGFAGALYWKX 239
 Db 180 TKPMP.LPVAASSLRNDSSSNRKAKNPGDSSLHMAAMALPALFSLIIGFAGALYWKX 240
 QY 240 QPSTLRAVENIQINEEDNEISMLQEKEREFQEV 273
 Db 240 QPSTLRAVENIQINEEDNEISMLQEKEREFQEV 274

RESULT 4

S47571
 stem cell factor, longer isoform - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 27-Jan-1995 #sequence_rev1sion 27-Jan-1995 #text_change 21-Jul-2000
 C:Accession: S47571
 R:Zhou, J.H.; Htkono, H.; Ohnaki, M.; Kubota, T.; Sakurai, M.
 Biochim. Biophys. Acta 1223, 148-150, 1994
 A:Title: Cloning and characterization of cDNAs encoding two normal isoforms of bovine st
 A:Reference number: S47571; MID:94339176; PMID:7520283
 A:Accession: S47571
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-274 <ZHO>
 A:Cross-references: EMBL:D28934; NID:9538520; PIDN:BA06061.1; PID:9538521
 C:Superfamily: mouse mast cell growth factor

Query Match 84.8%; Score 1184.5; DB 2; Length 274;
 Best Local Similarity 84.7%; Pred. No. 4e-86;
 Matches 232; Conservative 20; Mismatches 21; Indels 1; Gaps 1;

QY 1 MKKTQWTLITCTIYQLLEFPLVKTGICRRRTVNNVQVTKLVANLPKDYMITLKYPVG 60
 Db 1 MKKTQWTLITCTIYQLLEFPLVKTGICRRRTVNNVQVTKLVANLPKDYMITLKYPVG 60
 QY 61 MDVLPSCWISSEWVQSLDLDLDFKSNISEGLSNYSIIDKLVIIVDDIVECVKENS 120
 Db 61 MDVLPSCWISSEWVQSLDLDLDFKSNISEGLSNYSIIDKLVIIVDDIVECVKENS 120
 QY 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSV 179
 Db 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSV 180
 QY 180 TKPMP.LPVAASSLRNDSSSNRKAKNPGDSSLHMAAMALPALFSLIIGFAGALYWKX 239
 Db 180 TKPMP.LPVAASSLRNDSSSNRKAKNPGDSSLHMAAMALPALFSLIIGFAGALYWKX 240
 QY 240 QPSTLRAVENIQINEEDNEISMLQEKEREFQEV 273
 Db 240 QPSTLRAVENIQINEEDNEISMLQEKEREFQEV 274

RESULT 5

146929

stem cell factor - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 21-Jul-2000
C:Accession: I46929
R:Shull, R.M.; Suggs, S.V.; Langley, K.E.; Okino, K.H.; Jacobsen, F.W.; Martin, F.H.
Exp. Hematol. 20, 1118-1124, 1992
A:Title: Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic F
A:Reference number: I46929; MUID:93106145; PMID:1281786
A:Accession: I46929
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-274 <SHU>
A:Cross-references: GB:SS3329; NID:g262240; PTDN:AMB24619.1; PID:g262241
!Superfamily: mouse mast cell growth factor

Query	March	84.5%	Score	1180.5	DB	2	Length	274
Best	Local Similarity	85.4%	Pred.	No.8.2e-86				
Matches	234	Conservative	17	Mismatches	22	Indels	1	Gaps
Qy	1	MKKTQVWITLCIYIQLLLFNPLVKTGEGCRNRVTNNVADVTKLVAANLPKQYMTLTKAVPG	60					
Db	1	MKKQTWITTCIYIQLLLFNPLVKTGEGCRKRVTDVQVDTKLVAANLPKQYKILATKVPG	60					
Qy	61	MDVLPSSHQWISSEMYVQVSDSLTDLDDKPSNISEGINSYITDKYVNIYDVLVECKENSS	120					
Db	61	MDVLPSSHQWISVYMQQSVSLTDLDDKPSNISEGINSYITDKYKTVDDLVECTEGYSF	120					
Qy	121	KDLKSEFKSPPEPRLFTPEPEPRIFNRSIDAEPKDF-VYASSETSDCVSSTLSPKQSRVSY	179					
Db	121	ENVKAKAPSPELRLFTPEPEPRIFNRSIDAEPKDLLETVAASKSECVSSTLSPDQSRVSY	180					
Qy	180	TKRPMLPVAVAASSLRNSSSSNRKAKNPQGSILHMAAMALPALFSLIIGAFAPALYWK	239					
Db	181	TKRPMLPVAVAASSLRNSSSSNRKASNSIGSNILOMAAMALPALFSLVIGFAPALYWK	240					
Qy	240	ROPSTRAVENIQINEEDNEISMLQEKEREFOEV	273					
Db	241	KOPNLTTRVENIQINEEDNEISMLQEKEREFOEV	274					

RESULT 6
S65801
must cell growth factor - mouse
N:Alternate names: hematopoietic growth factor KL; ligand steel factor; stem cell factor
C:Species: Mus musculus (house mouse)
C:date: 28-Oct-1996 #sequence revision 27-Feb-1997 #text change 01-Dec-2000
C:Accession: S65801; A43751; A35976; A35977; A35972; A35975; A35973; I48768
R:Bebell, M.A.; Copeland, N.G.; Jenkins, N.A.
Genetics 142, 927-934, 1996
A:Title: Multiple pathways for Steel regulation suggested by genomic and sequence analysis
A:Reference number: S65801; MUID:97002551; PMID:884989
A:Accession: S65801
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-273 <BED>
A:Cross-references: EMBL:U044725; NID:g1172215; PID:AA052447.1; PID:g1172216
R:Hung, E.-J.; Nocka, K.H.; Buck, J.; Besmer, P.
Mol. Biol. Cell 3, 349-362, 1992
A:Title: Differential expression and processing of two cell associated forms of the kit
A:Reference number: A43751; MUID:92330001; PMID:1378327
A:Accession: A43751
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-214, 'L', 216-273 <HUA>
A:Cross-references: GB:S40364; NID:g251668; PID:AA022554.2; PID:g5705957
A:Note: the authors translated the codon TTG for threonine 215 as Trp
R:Hung, E.-J.; Nocka, K.H.; Beier, D.R.; Chu, T.Y.; Buck, J.; Lahn, H.W.; Wellner, D.; Ledet
Cell 63, 225-233, 1990
A:Title: The hematopoietic growth factor KL is encoded by the Sl locus and is the ligand
A:Reference number: A35976; MUID:91004221; PMID:1698557
A:Accession: A35976
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA

A:Residues: 1-206,'S',208-270 <H2>
A:Cross-references: GB:M38511
R:Anderson, D.M.; Lyman, S.D.; Baird, A.; Wignall, J.M.; Eisenman, J.; Rauch, C.; March
Cell 63, 235-243, 1990
A:Title: Molecular cloning of mast cell growth factor, a hematopoietic that is active in
A:Reference number: A35977; MUID:91004223; PMID:1698558
A:Accession: A35977
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-273 <AND>
A:Cross-references: GB:M57647; GB:M38436; NID:9199151; PIDN:AAA9358.1; PID:9199152
R:Kopeland, N.G.; Gilbert, D.J.; Cho, B.C.; Donovan, P.J.; Jenkins, N.A.; Cosman, D.; Ar
Cell 63, 175-183, 1990
A:Title: Mast cell growth factor maps near the steel locus on mouse chromosome 10 and is
A:Reference number: A35972; MUID:91004216; PMID:1698554
A:Accession: A35972
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 26-53 <COP>
A:Cross-references: GB:M59912
R:Seabo, K.M.; Williams, D.A.; Geisler, E.N.; Broudy, V.C.; Martin, F.H.; Ackins, H.L.
Cell 63, 213-224, 1990
A:Title: Stem cell factor is encoded at the Sl locus of the mouse and is the ligand for
A:Reference number: A35975; MUID:91004220; PMID:1698556
A:Accession: A35975
A:Molecule type: mRNA
A:Residues: 1-201 <ZSE>
A:Cross-references: GB:M59915; NID:9200935; PIDN:AAA40095.1; PID:9554271
R:Seabo, K.M.; Wyyck, J.; McNiece, I.K.; Lu, H.S.; Smith, K.A.; Karkare, S.B.; Sachdev,
A:Langley, K.E.
Cell 63, 195-201, 1990
A:Title: Identification, purification, and biological characterization of hematopoietic
A:Reference number: A35973; MUID:91004218; PMID:2208278
A:Accession: A35973
A:Status: preliminary
A:Molecule type: protein
A:Residues: 27-29,'R',31-39 <ZS2>
R:Brannan, C.I.; Bedell, M.A.; Resnick, J.L.; Eppig, J.J.; Handel, M.A.; Williams, D.E.
Genes Dev. 6, 1832-1842, 1992
A:Title: Developmental abnormalities in Steel^{17H} mice result from a splicing defect in t
A:Reference number: A44071; MUID:93012940; PMID:1383087
A:Accession: 148768
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-206,'S',208-273 <RES>
A:Cross-references: EMBL:X68989; NID:9395283; PIDN:CAA48778.1; PID:9395284
C:Genetics:
A:Gene: Slf
A:Map position: 10
C:Superfamily: mouse mast cell growth factor
C:Keywords: extracellular protein; glycoprotein; transmembrane protein

Query Match	82.8%;	Score 1157;	DB 2;	Length 273;
Best Local Similarity	82.8%;	Pred. No. 5.9e-84;		
Matches	226;	Conservative 19;	Mismatches 28;	Indels 0;
			Gaps 0;	
QY	1	MKKTQTMILITCIYQLLLFNPLVKEGICENRRVYNNKADYTKLVANLPKDYMITLKKVPV	60	
Db	1	MKKQTMITIITCIYQLLLFNPLVYKTKELCGNPATIDNVKDTIKLVANLPNDYMITLNVAG	60	
QY	61	MDVLPSCWISSEMYVQLSDSLTDLIDKFSNISSEGLSNYSIIIDKLVNIVDDLVECKENSS	120	
Db	61	MDVLPSCWLDWVYQLSLSTLTLLIDKFSNISSEGLSNYSIIIDKLGKIVDDLVCMEENAP	120	
QY	121	KDLKSFSPSPRLFTPEEFPRIFNRSIDAFKDPVVASETSDCVSVSTLSPEKDSRVSVT	180	
Db	121	KNIESPRPEPTRFTPEEFPFSIFNRSIDAFKDPVVASETSDCVSVSTLSPEKDSRVSVT	180	
QY	181	KPFMLPVVAASLLENDSSSNRRKAKNPGGDSLHMAAMALPALPSLIIGAFGALYKKR	240	
Db	181	KPFMLPVVAASLLENDSSSNRRKAKAPEDSGLOMTMALPALISLITVIGAFGALYKKK	240	

QY 241 QPSLTRAVERNIOQNEEDNEISMLQEKEREFQEV 273
 |||||
 Db 241 QSSLTRAVENIQNEEDNEISMLQEKEREFQEV 273

RESULT 7

mast cell growth factor precursor (version 2) - mouse
 A:Accession: A37934
 A:Molecule type: mRNA
 A:Residues: 1-245 <FLA>
 A:Cross-references: GB:M64262
 R: Huang, E.J.; Nocka, K.H.; Buck, J.; Besmer, P.
 Mol. Biol. Cell 3, 349-362, 1992
 A:Title: Differential expression and processing of two cell associated forms of the kit-
 A:Reference number: A43751; MUID:92330001; PMID:1378327
 A:Accession: B43751
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-173, 'R', 175-186, 'L', 188-245 <HUA>
 A:Cross-references: GB:S04534
 A:Note: the authors translated the codon TTG for residue 187 as Trp
 C:Superfamily: mouse mast cell growth factor

Query Match

Best Local Similarity 70.9%; Score 991; DB 2; Length 245;
 Matches 197; Conservative 19; Mismatches 29; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYPG 60
 |||||
 Db 1 MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISBEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDVLECKENSS 120
 |||||
 Db 61 MDVLPSCWISBEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDVLECKENSS 120
 QY 121 KDLKSFSPKPRPLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
 |||||
 Db 121 KDLKSFSPKPRPLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
 QY 181 KPFMLPPVAASLRNDSSSNRKAKNPQDSSSLHMAAMLPALFSLIIGFAGALYMKR 240
 |||||
 Db 181 KPFMLPPVAASLRNDSSSNRKAKNPQDSSSLHMAAMLPALFSLIIGFAGALYMKR 240
 QY 241 QPSLTRAVERNIOQNEEDNEISMLQEKEREFQEV 273
 |||||
 Db 241 QSSLTRAVENIQNEEDNEISMLQEKEREFQEV 273

RESULT 8

stem cell factor precursor - sheep (fragment)
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000
 C:Accession: S58313
 R:McInnes, C.J.; Logan, M.; Falconer, V.M.; Rawlins, P.; Huntly, J.; Haig, D.
 submitted to the EMBL Data Library, August 1995
 A:Description: Molecular cloning and biological activity of ovine stem cell factor.
 A:Reference number: S58313
 A:Accession: S58313
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-202 <MC1>
 A:Cross-references: EMBL:250743; NID:9940807; PIDN:CAA90620.1; PID:9940808
 C:Superfamily: mouse mast cell growth factor

Query Match 63.4%; Score 885.5; DB 2; Length 202;
 Best Local Similarity 86.1%; Pred. No. 1.1e-62;
 Matches 174; Conservative 15; Mismatches 12; Indels 1; Gaps 1;

QY 1 MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYPG 60
 |||||
 Db 1 MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISBEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDVLECKENSS 120
 |||||
 Db 61 MDVLPSCWISBEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDVLECKENSS 120
 QY 121 KDLKSFSPKPRPLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSV 179
 |||||
 Db 121 ENVKSSSPKPRPLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSV 180
 QY 180 TKPFMLPPVAASLRNDSSSN 201
 |||||
 Db 181 TKPFMLPPVAASLRNDSSSN 202

RESULT 9

stem cell factor protein precursor - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
 C:Accession: B35974; A39805
 R: Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.F.
 S, J.C.; Patel, A.C.; Fisher, E.F.; Ertavac, H.O.; Herrera, J.; Sachdev, R.
 Cell 63, 203-211, 1990
 A:Title: Primary structure and functional expression of rat and human stem cell factor D
 A:Reference number: A35974; MUID:91004219; PMID:2208279
 A:Accession: B35974
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-201 <MAR>
 A:Cross-references: GB:M59966; NID:9206861; PIDN:AAA42117.1; PID:9554507
 R: Lu, H.S.; Clogston, C.L.; Wypych, J.; Fausset, P.R.; Lauren, S.; Mendiaz, E.A.; Zsebo, J.
 Biol. Chem. 266, 8102-8107, 1991
 A:Title: Amino acid sequence and post-translational modification of stem cell factor iso
 A:Reference number: A39805; MUID:91217037; PMID:1708771
 A:Accession: A39805
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 'E', 27-190 <LUA>
 C:Superfamily: mouse mast cell growth factor

Query Match

Best Local Similarity 61.3%; Score 857; DB 2; Length 201;
 Matches 166; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYPG 60
 |||||
 Db 1 MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISBEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDVLECKENSS 120
 |||||
 Db 61 MDVLPSCWISBEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYDDVLECKENSS 120
 QY 121 KDLKSFSPKPRPLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
 |||||
 Db 121 KDLKSFSPKPRPLFTPEEPFRIFNRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
 QY 181 KPFMLPPVAASLRNDSSSN 201
 |||||
 Db 181 KPFMLPPVAASLRNDSSSN 201

RESULT 10

stem cell factor precursor - chicken
 C:Species: Gallus gallus (chicken)

A:Residues: 1-13;14-30;31-46;47-59;60-86;87-95;96-107;108-124 <LUH>
C:Superfamily: mouse mast cell growth factor

Job time : 16.4174 secs

Query Match 41.3%; Score 576.5; DB 2; Length 124;
Best Local Similarity 75.2%; Pred. No. 1.4e-38;
Matches 124; Conservative 0; Mismatches 0; Indels 41; Gaps 4;

QY 26 EGIARRVNNVNDVKLVANLPKDYMITLKYVPGMDVLPSCWISSEMYVQLSDSLTDLL 85
DB 1 EGIARRVNNVNDVKLVANLPKDYMITLKYVPGMDVLPSCWISSEMYVQLSDSLTDLL 30

QY 86 DKFSNISSEGLSNYSIIDKLVNIVDLVECVKENSCKLKKSPKPPRLFTPEEFRIEN 145
DB 31 DKFSNISSEGLSNYSIIDKLVNIVDLVECVKENSCKLKKSPKPPRLFTPEEFRIEN 83

QY 146 RSLDAKDFVAVASSETSDCVVSSSTLSPKDSRVSVTKPFMLPPVAA 190
DB 84 RSLDAKDFVAVASSETSDCVVSSSTLSPKDSRVSVTKPFMLPPVAA 124

RESULT 14

B35971
mast cell growth factor - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000

C:Accession: B35971

R:Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I.
Cell 63, 167-174, 1990

A:Title: Identification of a ligand for the c-kit proto-oncogene.

A:Reference number: A35971; MUID:91004215; PMID:1698553

A:Accession: B35971

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-51 <WIL>

C:Superfamily: mouse mast cell growth factor
C:Keywords: transmembrane protein

Query Match 12.6%; Score 175.5; DB 2; Length 51;
Best Local Similarity 72.3%; Pred. No. 1.9e-07;

Matches 34; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 28 ICRNRVTNNVKDVTKLVANLPKDYMITLKYVPGMDVLPSCWISSEMY 74
DB 3 ICRNPVTNNVKDVTKLVANLPKDYMITLKYVPGMDVLPSCWISSEMY 48

RESULT 15

A35971

mast cell growth factor - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000

C:Accession: A35971

R:Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I.
Cell 63, 167-174, 1990

A:Title: Identification of a ligand for the c-kit proto-oncogene.

A:Reference number: A35971; MUID:91004215; PMID:1698553

A:Accession: A35971

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-49 <WIL>

C:Superfamily: mouse mast cell growth factor
C:Keywords: transmembrane protein

Query Match 12.3%; Score 172.5; DB 2; Length 49;
Best Local Similarity 73.5%; Pred. No. 3e-07;
Matches 36; Conservative 4; Mismatches 6; Indels 3; Gaps 2;

QY 28 ICRNRVTNNVKDVTKLVANLPKDYMITLKYVPGMDVLPSCWISSEMY 76
DB 3 ICRNPVTNNVKDVTKLVANLPKDYMITLKYVPGMDVLPSCWISSEMY 48

Search completed: February 5, 2004, 15:08:21

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 14:42:38 ; Search time 8.64876 Seconds
(without alignments)
1484.408 Million cell updates/sec

Title: US-09-224-683-61

Perfect score: 1397

Sequence: 1 MKKTQWILTCIYLQLLFN.....NEEDNEISMLQEKEREQEV 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1397	100.0	273	1 SCF_HUMAN	P21583 homo sapien
2	1219.5	87.3	274	1 SCF_HORSE	Q95md2 equus caball
3	1217.5	87.2	274	1 SCF_FELCA	P79169 felis silve
4	1203.5	86.1	274	1 SCF_PIG	Q29030 sus scrofa
5	1187.5	85.0	274	1 SCF_CAPIH	Q95m19 capra hircu
6	1184.5	84.8	274	1 SCF_BOVIN	Q28132 bos taurus
7	1180.5	84.5	274	1 SCF_CANFA	Q06220 canis famli
8	1180.5	84.5	274	1 SCF_MUSVI	Q95n18 muscicola vis
9	1158	82.9	273	1 SCF_RAT	P21581 rattus norv
10	1157	82.8	273	1 SCF_MOUSE	P20826 mus musculu
11	1156.5	82.8	267	1 SCF_SHEEP	P79368 ovis aries
12	703	50.3	287	1 SCF_CHICK	Q09108 gallus gall
13	702	50.3	287	1 SCF_CONVA	Q90314 coturnix co
14	107.5	7.7	989	1 PTP3_DICDI	P54637 dictyosteli
15	97.5	7.0	403	1 RAGE_MOUSE	Q62151 mus musculu
16	97	6.9	981	1 SCFA_MOUSE	Q94337 rickettsia
17	96.5	6.9	1742	1 MYSC_HUMAN	Q94q44 homo sapien
18	93.5	6.7	1813	1 UN13_CABEL	P27715 caenorhabdi
19	91.5	6.5	496	1 MURE_WIGBR	Q8d21 wi99lewort
20	90.5	6.5	1932	1 FABI_SCHPO	Q59722 schizosacch
21	90	6.4	378	1 FDHA_MERUA	Q60314 methanococc
22	89.5	6.4	384	1 NRRF_HAEIN	P44942 haemophilus
23	89	6.4	282	1 Y218_RICPR	Q05944 rickettsia
24	89	6.4	998	1 SC4A_RICAK	Q9a199 rickettsia
25	88.5	6.3	1325	1 YAB6_SCHPO	Q09847 schizosacch
26	88.5	6.3	1875	1 MLPI_YEAST	Q02445 saccharomyc
27	88	6.3	449	1 Y865_MERUA	Q59825 methanococc
28	88	6.3	742	1 YAKH_SCHPO	Q09932 schizosacch
29	87.5	6.3	966	1 CAPF_MERUA	Q02735 medicago sa
30	87	6.2	402	1 RAGE_RAT	Q63455 rattus norv
31	87	6.2	469	1 C39A_HUMAN	Q9ny15 homo sapien
32	87	6.2	664	1 ZAAA_CAEEL	Q09543 caenorhabdi
33	87	6.2	844	1 BRO1_YEAST	P48582 saccharomyc

34	87	6.2	1202	1	YE01_SCHPO	O13798 schizosacch
35	86.5	6.2	410	1	ARCA_BORBU	O51781 borellia bu
36	86.5	6.2	451	1	DNNA_PASMU	O9c1q4 baetereilla
37	86.5	6.2	466	1	DNNA_PROMI	P22837 proteus mir
38	86.5	6.2	545	1	VNCS_UCDNV	Q90054 junonia coe
39	86.5	6.2	729	1	CUD6_CAEEL	Q21346 caenorhabdi
40	86.5	6.2	1675	1	POL_RTBVP	P27502 rice tungro
41	86.5	6.2	2492	1	TALA_DICDI	P54633 dictyosteli
42	86	6.2	991	1	SC4A_RICAU	Q9a164 rickettsia
43	86	6.2	1146	1	KHMA_DICDI	P42527 dictyosteli
44	86	6.2	2238	1	RRPL_BUNYM	P20470 bunyameira
45	85.5	6.1	344	1	ETPA_YEAST	O12480 saccharomyc

ALIGNMENTS

RESULT 1	ID	SCF_HUMAN	STANDARD:	PRT:	273 AA.
AC	P21583	Q16487; Q9UOK7;			
DT	01-MAY-1991	(Rel. 18, Created)			
DT	01-MAY-1991	(Rel. 18, Last sequence update)			
DT	15-SEP-2003	(Rel. 42, Last annotation update)			
DE	Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).				
GN	KITLG OR MGF OR SCF				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 1)				
RX	MEDLINE=91004219; PubMed=2208279;				
RA	Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,				
RA	Morris C.F., McNeice I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,				
RA	Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,				
RA	Fisher B.F., Erjavec H.O., Herrera C.J., Wyrzycki J., Sachdev R.K.,				
RA	Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zeebo K.M.,				
RT	"Primary structure and functional expression of rat and human stem				
RT	cell factor DNAs."				
RL	Cell 63:203-211(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM 2)				
RX	MEDLINE=99160429; PubMed=10049787;				
RA	Blair H.C., Julian B.A., Cao X., Jordan S.E., Dong S.S.,				
RA	"Parathyroid hormone-regulated production of stem cell factor in human				
RT	osteoblasts and osteoblast-like cells."				
RL	Biochem. Biophys. Res. Commun. 255:778-784(1999).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RA	Han C., Peng X., Yuan J., Qiang B.,				
RA	Submitted (Jul-2001) to the EMBL/Genbank/DBJ databases.				
RN	[4]				
RP	SEQUENCE OF 167-248 FROM N.A. (ISOFORM 2).				
RX	MEDLINE=92360843; PubMed=1379846;				
RA	Toyota M., Hineda Y., Itoh F., Tsujisaki M., Inai K., Yachi A.,				
RA	"Expression of two types of kit ligand mRNAs in human tumor cells."				
RL	Int. J. Hematol. 55:301-304(1992).				
CC	-1- FUNCTION: Stimulates the proliferation of mast cells. Able to				
CC	augment the proliferation of both myeloid and lymphoid				
CC	hematopoietic progenitors in bone marrow culture. Mediates also				
CC	cell-cell adhesion. Acts synergistically with other cytokines,				
CC	probably interleukins.				
CC	-1- SUBUNIT: Homodimer, non-covalently linked (Probable).				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).				
CC	Also exists as a secreted soluble form (isoform 1 only) (By				
CC	similarity).				
CC	-1- ALTERNATIVE PRODUCTS:				
CC	Event=Alternative splicing; Named isoforms=2;				
CC	Name=1; Synonyms=SCF248;				
CC	Isoid=P21583-1; Sequence=Displayed;				
CC	Name=2; Synonyms=SCF220;				

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CC      IsoId=P21583-2; Sequence=VSP_006022;
CC      -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC      -1- PTM: A soluble form is produced by proteolytic processing of
CC      isoform 1 in the extracellular domain.
CC      -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC      -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC      WWW="http://www.infobiogen.fr/services/chromosome/Genes/MGFD142.html".
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      use by non-profit institutions as long as its content is in no way
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; MS9564; AAA65450.1; -
CC      EMBL; AF119835; AAD2048.1; -
CC      EMBL; AF400436; AAK92485.1; -
CC      EMBL; AF400437; AAK92486.1; -
CC      EMBL; S42571; AAB22846.2; -
CC      PIR; A35974; A35974.
CC      PIR; B61190; B61190.
CC      GeneW; HGNC:6343; KITLG.
CC      NIM; 184745; -
CC      DR CO; GO:0005173; F:stem cell factor receptor binding activity; TAS.
CC      DR CO; GO:0008283; P:cell proliferation; TAS.
CC      DR GO; GO:0007165; P:signal transduction; TAS.
CC      DR InterPro; IPR003452; SCF.
CC      DR Pfam; PF02404; SCF; 1.
CC      KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
CC      Alternative splicing.
CC      FT SIGNAL 1 25
CC      FT CHAIN 26 273
CC      FT DOMAIN 26 214
CC      FT TRANSMEM 215 237
CC      FT DOMAIN 238 273
CC      FT DISULFID 29 114
CC      FT CARBOHYD 68 163
CC      FT CARBOHYD 97 90
CC      FT CARBOHYD 97 97
CC      FT CARBOHYD 118 118
CC      FT CARBOHYD 145 145
CC      FT CARBOHYD 195 195
CC      FT VARSPPLIC 174 202
CC      isofrm 2).
CC      /FTID=VSP_006022.
CC      FT CONFLICT 55 55
CC      FT CONFLICT 128 128
CC      FT CONFLICT 134 134
CC      FT CONFLICT 134 134
CC      SQ SEQUENCE 273 AA; 30898 MW; 19FD362CB59C6607 CRC64;
CC      -----
CC      Query Match 100.0%; Score 1397; DB 1; Length 273;
CC      Best Local Similarity 100.0%; Pred. No. 3.7e-100;
CC      Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      241 OPLTRAVENIQINEDNEISMLQEKERFQEV 273
|||||
RESULT 2
SCF_HORSE
ID SCF_HORSE STANDARD; PRT; 274 AA.
AC 095MD2; 062765; 095MG8; Q9N1V5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kit ligand precursor (C-Kit ligand) (stem cell factor) (SCF) (mast
DE cell growth factor) (MGF).
GN KITLG OR MGF OR SCF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE OF 4-264 FROM N.A.
RA Terry R.R., Mickelson J.R., Schmutz S., Cotran E.G., Bailey E.;
RT "Equus caballus mast cell growth factor (MGF).";
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 12-267 FROM N.A.
RA Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.;
RT "An Equine sequence homologous to stem cell factor (KIT-ligand).";
RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE OF 107-202 AND 227-274 FROM N.A.
RA Terry R.R., Bailey E.F., Cotran E.G.;
RT "Evaluation of MGF as the candidate gene for Appaloosa spotting.";
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 147-197 FROM N.A.
RA Caetano A.R., Shue Y.-L., Lyons L.A., Laughlin T.F., O'Brien S.J.,
RA Murray J.D., Bowling A.T.;
RT "A primary Human-Horse comparative gene map.";
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
CC augment the proliferation of both myeloid and lymphoid
CC hematopoietic progenitors in bone marrow culture. Mediates also
CC cell-cell adhesion. Acts synergistically with other cytokines,
CC probably interleukins (By similarity).
CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
CC secreted soluble form (By similarity).
CC -1- PTM: A soluble form is produced by proteolytic processing of
CC the extracellular domain (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; AF401625; AAK94474.1; -
CC      EMBL; AF053498; AAC97076.1; -
CC      EMBL; AF367704; AAK63249.1; -
CC      EMBL; AF367706; AAK63250.1; -
CC      EMBL; AF130770; AAK63716.1; -
CC      InterPro; IPR003452; SCF.
CC      Pfam; PF02404; SCF; 1.
CC      KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
CC      FT SIGNAL 1 25
CC      FT CHAIN 26 274
CC      FT DOMAIN 26 215
CC      FT TRANSMEM 216 238
CC      FT DOMAIN 239 274
CC      CYTOPLASMIC (POTENTIAL).

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FT	DISULFID	29	114	BY SIMILARITY.
FT <td>DISULFID</td> <td>68</td> <td>164</td> <td>BY SIMILARITY.</td>	DISULFID	68	164	BY SIMILARITY.
FT	CARBOHYD	90	90	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	97	97	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	145	145	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	196	196	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	207	207	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	15	15	Q -> P (IN REF. 2).
FT	CONFLICT	241	241	MISSING (IN REF. 3).
SO	SEQUENCE	274 AA;	31217 MM;	96C1D4C9059132F2 CRC64;
Query Match				
Best Local Similarity		87.3%;	Score 1219.5;	DB 1; Length 274;
Matches		239;	Conservative	19; Mismatches 15; Indels 1; Gaps 1
Qy	1	MKKQTWILTCIYQDLLFNPLVKTGECIRNRVTNNVXDVTKLVANLPKDYMTLKYVP	60	
Db	1	MKKQTWILTCIYQDLLFNPLVKTGECIRNRVTNNVXDVTKLVANLPKDYMTLKYVP	60	
Qy	61	MDVLPSCHWISBWMVQSLDSDLTDLDKSNISBEGSNYSIIDKLVNIYDDLYCEKENS	120	
Db	61	MDVLPSCHWISBWMVQSLDSDLTDLDKSNISBEGSNYSIIDKLVNIYDDLYCEKENS	120	
Qy	121	KDLKSPSPPEPLTPEPEPFIENRSIDAFKDF-VVASSETSDCVSSTLSPKDSRSV	179	
Db	121	ENVKSYSSQESRLTPEPEPFIENRSIDAFKDFLWVSKSECVSSTLSPKDSRSV	180	
Qy	180	TKPEFLPVAASSLRNDSSSSNRKAKNPGDSSLHMAAMALPALFSLITGAFGALYMK	239	
Db	181	TKPEFLPVAASSLRNDSSSSNRKAKNPGDSSLHMAAMALPALFSLITGAFGALYMK	240	
Qy	240	ROPSTRAVENIQINEEDNEISMLOEKEREFOEV	273	
Db	241	KOPNLTRAVENIQINEEDNEISMLOEKEREFOEV	274	
RESULT 3				
SCF_FELCA	ID	SCF_FELCA	STANDARD;	PRT; 274 AA.
AC	P79169;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).			
GN	KITLG OR SCF.			
OS	Felis silvestris catus (Cat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.			
OX	NCBI_TaxID=9685;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RX	MEDLINE=97069946; PubMed=8912926;			
RA	Dunham S.P., Onions D.E.;			
RT	"The cloning and sequencing of cDNAs encoding two isoforms of feline stem cell factor."			
RL	DNA Seq. 6:233-237(1996).			
CC	-1- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).			
CC	-1- SUBUNIT: Homodimer, non-covalently linked (Probable).			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2). Also exists as a secreted soluble form (isoform 1 only) (By similarity).			
CC	-1- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=2;			
CC	Name=1;			
CC	Isoid=P79169-1; Sequence=Displayed;			
CC	Name=2;			
CC	Isoid=P79169-2; Sequence=VSP_006021;			
CC	-1- PTM: A soluble form is produced by proteolytic processing of			

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CC isoform 1 in the extracellular domain (By similarity).
CC
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
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CC -----
CC DR EMBL; D50833; BAA09445.1; -.
CC DR InterPro: IPR003452; SCF.
CC DR Pfam; PF02404; SCF. 1.
CC KW Growth factor; Glycoprotein; Transmembrane; signal; Cell adhesion;
CC KM Alternative splicing.
CC FT SIGNAL 1 25 POTENTIAL.
CC FT CHAIN 26 274 KIT LIGAND.
CC FT DOMAIN 26 215 EXTRACELLULAR (POTENTIAL).
CC FT TRANSEM 216 238 POTENTIAL.
CC FT DOMAIN 239 274 CYTOPLASMIC (POTENTIAL).
CC FT DISULFID 29 114 BY SIMILARITY.
CC FT DISULFID 68 164 BY SIMILARITY.
CC FT CARBOHYD 97 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT VARSPLIC 175 203 DSRVSVTKPMPMLPPVAASSLRNDSSSNR -> G (1n
CC isoform 2).
CC FT /FTID:VSP 006021.
CC SQ SEQUENCE 274 AA; 30987 MW; C5B78DB84791237BE CRC64;
CC
CC Query Match 87.2%; Score 1217.5; DB 1; Length 274;
CC Best Local Similarity 87.2%; Pred. No. 2.1e-86;
CC Matches 239; Conservative 17; Mismatches 17; Indels 1; Gaps 1;
CC
CC QY 1 MKKTQWTLFTCIYQLLFPNPLYKTSGICNNRRVTNNYKDYTKLVANPKDYMTLTAKYVP 60
CC DB 1 MKKTQWTLFTCIYQLLFPNPLYKTSGICNNRRVTNNYKDYTKLVANPKDYMTLTAKYVP 60
CC
CC QY 61 MDVLPSSHCHSWMEVQSVSLTDLDFENISBSLSNYSTIIDKLVNIVDDLVEGVKENS 120
CC DB 61 MDVLPSSHCHSWMEVQSVSLTDLDFENISBSLSNYSTIIDKLVNIVDDLVEGVKENS 120
CC
CC QY 121 KDLKSKFSPEPRLLFTPEEFPRIFNRSIDAFKDF-VVAESTSDCVSVSTLSPKDSRVSV 179
CC DB 121 KDLKSKFSPEPRLLFTPEEFPRIFNRSIDAFKDF-VVAESTSDCVSVSTLSPKDSRVSV 179
CC
CC QY 121 ENYKSSKSGSEPRLLFTPEEFPRIFNRSIDAFKDLQEWAKSTSECVSVSTLSPKDSRVSV 180
CC DB 121 ENYKSSKSGSEPRLLFTPEEFPRIFNRSIDAFKDLQEWAKSTSECVSVSTLSPKDSRVSV 180
CC
CC QY 180 TKCPMLPPVAASSLRNDSSSNRKAKNPQDSSLIHMAAMALPALFSIIIGFAGALYWK 239
CC DB 181 TKCPMLPPVAASSLRNDSSSNRKAKNPQDSSLIHMAAMALPALFSIIIGFAGALYWK 240
CC
CC QY 240 RQSLPLRAVENIQINEEDNEISMLQEKEREFQEV 273
CC DB 241 RQSLPLRAVENIQINEEDNEISMLQEKEREFQEV 274
CC
CC RESULT 4
CC SCF_PIG STANDARD; PRT; 274 AA.
CC ID_SCF_PIG AC Q29030;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast
CC cell growth factor) (MGF).
CC GN KITLG OR MGF.
CC OS Sus scrofa (Pig).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CC NX NCBI_TaxID=9623;
CC NP [1]
CC SEQUENCE FROM N.A.

```

RC	TX	TISSUE=Uterus;	MEDLINE=94146218; PubMed=7508758;
RA	Zhang Z., Anthony R.V.;	"Porcine stem cell factor/c-kit ligand: its molecular cloning and localization within the uterus.";	RT
RL	Biol. Reprod. 50:95-102(1994).	-I- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).	CC
CC	-I- SUBUNIT: Homodimer, non-covalently linked (Probable).	-I- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).	CC
CC	-I- PIM: A soluble form is produced by proteolytic processing of the extracellular domain (By similarity).	-I- SIMILARITY: BELONGS TO THE SCF FAMILY.	CC
CC	-I- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-stb.ch/announce/ or send an email to license@isb-stb.ch).		CC
DR	EMBL; L07786; AAA53670.1; -.		DR
DR	PIR; I46575; I46575.		DR
DR	InterPro; IPR003452; SCF.		DR
DR	Pfam; PF02404; SCF; 1.		DR
KW	Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.		KW
FT	SIGNAL	1 25	FT
FT	CHAIN	26 274	FT
FT	DOMAIN	26 215	FT
FT	TRANSMEM	216 238	FT
FT	DOMAIN	239 274	FT
FT	DISULFID	29 114	FT
FT	DISULFID	68 164	FT
FT	CARBOHYD	90 90	FT
FT	CARBOHYD	97 97	FT
FT	CARBOHYD	145 145	FT
FT	CARBOHYD	196 196	FT
FT	SEQUENCE	274 AA; 3118 MW; FP3C87114D7BA6A6 CRC64;	FT
Query Match	Best Local Similarity	86.1%; Score 1203.5; DB 1; Length 274;	
Matches 235; Conservative	22; Mismatches 16; Indels 1; Gaps 1;		
OY	1 MKKTQWTALTCIYQDLFLNPLVYKTEGICRRNRVNNVQDVKLVANLPKDYMITLKYPG 60		OY
Db	1 MKKTQWTALTCIYQDLFLNPLVYKTEGICRRNRVNNVQDVKLVANLPKDYMITLKYPG 60		Db
OY	61 MDVLPSSHCHISEMVAQSDSLTDLIDKRSNISEGINSYIIDKLVNIYDDLVCEKENS 120		OY
Db	61 MDVLPSSHCHISEMVAQSDSLTDLIDKRSNISEGINSYIIDKLVNIYDDLVCEKENS 120		Db
OY	121 KDLKSKFSPEPRLLFTPEEFRIFRNSIDAERDF-VVASETSDCVSSSTISPEKDSRVSV 179		OY
Db	121 ENVKSSKSPPEPRLLFTPEEFRIFRNSIDAERDF-VVASETSDCVSSSTISPEKDSRVSV 180		Db
OY	180 TKPFLMPVVAASGLRNDSSSSNRKAKNDPGSSLHMAAMALPALPSLITGFAFALYWK 239		OY
Db	181 TKPFLMPVVAASGLRNDSSSSNRKAKNDPGSSLHMAAMALPALPSLITGFAFALYWK 240		Db
OY	240 RQPSLTRAVENTIOINEEDNEISMLQEKREPOEV 273		OY
Db	241 KQPNLIRTVENIQINEEDNEISMLQEKREPOEV 274		Db
RESULT 5	SCF CAPHI	STANDARD; PRT; 274 AA.	
ID	SCF CAPHI		
AC	Q95M19;		

```

DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cell ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast
DE cell growth factor) (MGF).
RT K1TG OR SCF.
RN Capra hircus (Goat).
OS Capra hircus
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Shiba; TISSUE=Brain;
RA Yamagawa N., Tanaka S., Yamanouchi K., Tojo H., Tachi C.;
RT "Identification of splicing isoforms of caprine stem cell factor
RT (gSCF) transcripts and expression patterns of the two major isoforms,
RT gSCF825 and gSCF741, in the brain and the skin of adult and fetal
RT Shiba goats." Capra hircus ";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Stimulates the proliferation of mast cells. Able to
CC augment the proliferation of both myeloid and lymphoid
CC hematopoietic progenitors in bone marrow culture. Mediates also
CC cell-cell adhesion. Acts synergistically with other cytokines,
CC probably interleukins (By similarity).
CC -I- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
CC secreted soluble form (By similarity).
CC -I- PTM: A soluble form is produced by proteolytic processing of
CC the extracellular domain (By similarity).
CC -I- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
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CC or send an email to license@isb-stb.ch).
CC -----
DR EMBL; AB002152; BAB71753.1; -.
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
DR Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
FT SIGNAL 1 25
FT CHAIN 26 274
FT DOMAIN 26 215 KIT LIGAND.
FT TRANSMEM 216 238 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 239 274 POTENTIAL.
FT DISULFID 29 114 CYTOPLASMIC (POTENTIAL).
FT DISULFID 68 164 BY SIMILARITY.
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 274 AA; 31052 MW; BBE669A09EF65D CRC64;
Query Match 85.0%; Score 1187.5; DB 1; Length 274;
Best Local Similarity 85.0%; Pred. No. 4.3e-84;
Matches 233; Conservative 20; Mismatches 20; Indels 1; Gaps 1
QY 1 MKKTQWILTCIYQLLLFNPLVTEGICRNRVNNVADVTKLVANLPKQYMITLKVYG 60
QY 1 MKKTQWILTCIYQLLLFNPLVTEGICRNRVNNVADVTKLVANLPKQYMITLKVYG 60
DB 1 MKKTQWILTCIYQLLLFNPLVHSGICRNRVADVTKLVANLPKQYMITLKVYG 60
QY 61 MDVLPSCHWSENVVQVSDSLTDLIDKFSNISSEGLSNYSIIDKLVNYVDLVECYKENSS 120
QY 61 MDVLPSCHWSENVVQVSDSLTDLIDKFSNISSEGLSNYSIIDKLVNYVDLVECYKENSS 120
DB 61 MDVLPSCHWSENVQVSLTDLIDKFSNISSEGLSNYSIIDKLVNYVDLVECYKERSF 120
QY 121 KDLKKSFSPEPRPLFTEPEEPRIFNRSIDAVKDF-VVASETSPDCVASTLSPKDSRVSV 179
QY 121 KDLKKSFSPEPRPLFTEPEEPRIFNRSIDAVKDF-VVASETSPDCVASTLSPKDSRVSV 179
DB 121 ENVAKSKSPPEPRPTFEKFFGINKKSIDAFKDLFIIVASTMSECVISTSSPEKDSRVSV 180

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Query Match	Best Local Similarity	84.5% Matches 234;	Score 1180.5; Pred. No. 1.5e-83;	DB 1; Indels 1;	Length 274; Gaps 1;
RA	"Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic progenitors in long-term canine marrow culture."				
RT	Exp. Hematol. 20:1118-1124(1992).				
RL	[2]				
RN	SEQUENCE OF 17-274 FROM N.A.				
RP	TISSUE=Tall;				
RA	Schmütz S.M., Berryere T.G.;				
RL	"MCP sequencing in the dog aids in mapping to CP415."				
CC	Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.				
CC	- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins.				
CC	- SUBUNIT: Homodimer, non-covalently linked (Probable).				
CC	- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form.				
CC	- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.				
CC	- PFM: A soluble form is produced by proteolytic processing of the extracellular domain (By similarity).				
CC	- SIMILARITY: BELONGS TO THE SCF FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use. By non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; S53329; AAB24619.1; -				
DR	EMBL; AY094361; AAM16280.1; -				
DR	PIR; I46929; I46929.				
DR	InterPro; IPR003452; SCF.				
DR	Pfam; PF02404; SCF; 1.				
KM	Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.				
FT	SIGNAL 1 25 BY SIMILARITY.				
FT	CHAIN 26 274 KIT LIGAND.				
FT	DOMAIN 26 215 EXTRACELLULAR (POTENTIAL).				
FT	TRANSMEM 216 238 POTENTIAL.				
FT	DOMAIN 239 274 CYTOPLASMIC (POTENTIAL).				
FT	DISULFD 29 114 BY SIMILARITY.				
FT	DISULFD 68 164 BY SIMILARITY.				
FT	CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD 146 196 N-LINKED (GLCNAC. . .) (POTENTIAL).				
SO	SEQUENCE 274 AA; 30869 MW; 4182BE9AED00793B CRC64;				

RESULT:	8			
ID	-SCF MUSVI	STANDARD;	PRT;	274 AA.
AC	Q95N18; Q95NM5;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).			
DE	Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).			
GN	KITLG OR SCF.			
OS	Musclea yvon (American mink).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;			
OC	Mustela.			
OX	NCBI_TaxID=9667;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RA	Bennett R.D., Murphy B.D.;			
RL	Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.			
CC	-I- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, particularly interleukins (By similarity).			
CC	-I- SUBUNIT: Homodimer, non-covalently linked (Probable).			
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).			
CC	-I- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=2;			
CC	Name=1;			
CC	IsoId=G95N18-1; Sequence=Displayed;			
CC	Name=2;			
CC	IsoId=G95N18-2; Sequence=VSP_006024;			
CC	-I- PTM: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain (By similarity).			
CC	-I- SIMILARITY: BELONGS TO THE SCF FAMILY.			
CC	-----			
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CC	-----			
DR	EMBL; AY013712; AACG7434.1; .			
DR	EMBL; AF323757; AAK73366.1; .			
DR	InterPro; IPR003452; SCF.			
DR	Pfam; PF02404; SCF; 1.			
KW	Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;			
KW	Alternative splicing.			
FT	SIGNAL	1	25	
FT	CHAIN	26	274	
FT	DOWAIN	26	215	
FT	TRANSMEM	216	238	
FT	DOWAIN	239	274	
FT	DISULFID	29	114	
FT	DISULFID	68	164	
FT	CARBOHYD	90	90	
FT	CARBOHYD	97	97	
FT	CARBOHYD	145	145	
FT	CARBOHYD	196	196	
FT	VASPELIC	175	203	
FT	/FtId=VSP_006024.			
FT	S->P (IN REF. 1; AAK73366).			
FT	S->N (IN REF. 1; AAK73366).			
FT	EREROEV->RSFRKCNCGPFHTVLVSIVGG (IN REF. 1; AAK73366).			
SE	SEQUENCE	274 AA;	31034 MM;	SAC1619014E5E72 CRC64;

Query Match 84.5%; Pred. 1180.5; DB 1; Length 274;
Best Local Similarity 84.3%; Prec. NO.15e-83;
Matches 231; Conservative 20; Mismatches 22; Indels 1; Gaps 1

QY 1 MKKTQTWLTTCIYDQLLEFNPLVKEGICRRNVTNNVVDKTLVNLPRQYMITLKRYVG 60
Db 1 MKKTQTWLTTCIYDQLLEFNPLVLRKGI CRRNVTVDVQDVTGLVNLPRDYKIALTYVPG 60

QY 61 MDVLPSSHWSBEMVQVLSLTDLLDKRNSISEGLSNYSIDKL VNIYVDLVECKENSS 120
Db 61 MDVLSHHCWIMVMEQVLSLTDLLDKRNSISEGLSNYSIDKL VKIYVDLVECKEHS 120

QY 121 KDILKSEKSPPEPLPTPEEPFPIENRSDAFKDF-VVASETSDCVSSSTLSEKDSRSV 179
Db 121 ENVKSSPNPDEPRHAPDFPFPIENRSDIDLKDLTAVASKTSECVLPSTLSEKDSRSV 180

QY 180 TKPPEMLPVAASSLNDSSSNRKKANPPGDSLHWAMALPALFSLIGAFGALYWK 239
Db 181 TKPPEMLPVAASSLNDSSSNRKKANPLGDSNLOAMAMALPAFSLVIGFAFGALYWK 240

QY 240 RQPSLTRAVENIQINEEDNEISMLOEKEREPOEV 273
Db 241 KQPNLTRAVENIQINEEDNEISMLOEKEREPOEV 274

RESULT 9
SCF_RAT
ID SCF_RAT STANDARD; PRT; 273 AA.
AC P21581; Q9QWZ4; Q9Z2E7;
DT 01-MAY-1991 (Rel. 18. Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Klt ligand precursor (C-klt ligand) (stem cell factor) (SCF) (Mast
DE cell growth factor) (MCF) (hematopoietic growth factor KL).
DE KIRITG OR MGF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Teramoto T., Nagashima M., Thorgeirsson S.S.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-201 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91004219; PubMed=2208279;
RA Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Tung J., Okino K.H.,
RA Morris C.F., McNeiece I.K., Jacobson F.W., Mendiaz E.A., Birkett N.C.,
RA Smith K.A., Johnson M.U., Parker V.P., Flores J.C., Patel A.C.,
RA Fisher E.F., Ertelavac H.O., Herrera C.J., Wypych J., Sachdev R.K.,
RA Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zeebo K.M.;
RT "Primary structure and functional expression of rat and human stem
RT cell factor DNAs.";
RL Cell 63:203-211(1990).
RN [3]
RP SEQUENCE OF 26-190, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX STRAIN=Buffalo; TISSUE=Liver;
RX MEDLINE=91217037; PubMed=1708771;
RA Lu H.S., Clogston C.L., Wypych J., Fausset P.R., Lauren S.,
RA Mendiaz E.A., Zeebo K.M., Langley K.E.;
RT "Amino acid sequence and post-translational modification of stem cell
RT factor isolated from buffalo rat liver cell-conditioned medium.";
RL J. Biol. Chem. 266:8102-8107(1991).
RN [4]
RP SEQUENCE OF 26-39.
RX MEDLINE=91004218; PubMed=2208278;
RA Zeebo K.M., Wypych J., McNeiece I.K., Lu H.S., Smith K.A.,
RA Karkare S.B., Sachdev R.K., Yushchenko V.N., Birkett N.C.,
RA Williams L.R., Satyagali V.N., Tung W., Bosseman R.A., Mendiaz E.A.,
RA Langley K.E.;
RT "Identification, purification, and biological characterization of
RT hematopoietic stem cell factor from buffalo rat liver-conditioned
RT medium.";

```

Rt Cell 63:195-201(1990).
CC -I- FUNCTION: Stimulates the proliferation of mast cells. Able to
CC augment the stimulation of both myeloid and lymphoid
CC hematopoietic progenitors in bone marrow culture. Mediates also
CC cell-cell adhesion. Acts synergistically with other cytokines,
CC probably interleukins.
CC -I- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2) .
CC Also exists as a secreted soluble form (isoform 1 only) (By
CC similarity).
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ku-1;
CC IsoId=P21581-1; Sequence=Displayed;
CC Name=2; Synonyms=Ku-2;
CC IsoId=P21581-2; Sequence=VSP_006025;
CC -I- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC -I- PIM: A soluble form is produced by proteolytic processing of
CC isoform 1 in the extracellular domain.
CC -I- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
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CC -----
DR EMBL; AF071204; AAD02827.1; -.
DR EMBL; AF071205; AAD02828.1; -.
DR EMBL; M59966; AAA42117.1; -.
DR PIR; B35974; B35974.
DR InterPro; IPRO03452; SCF.
DR Pfam; PF02404; SCF.1.
DR Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
KW Alternative splicing; Pyroglutamate carboxylic acid.
KM
FT SIGNAL 1 25
FT CHAIN 26 273
FT DOMAIN 26 214
FT TRANSMEM 215 237
FT DOMAIN 238 273
FT MOD_RES 26 26
FT DISULFD 29 114
FT CARBOHYD 68 163
FT CARBOHYD 90 90
FT CARBOHYD 145 145
FT CARBOHYD 167 167
FT CARBOHYD 168 168
FT CARBOHYD 180 180
FT CARBOHYD 195 195
FT VARSPLIC 174 202
FT FT
FT FT
FT FT
FT FT
SQ SEQUENCE 207 207
273 AA; 30712 MW; 3CF56527DC93FD27 CRC64;

Query Match 82.9%; Score 1158; DB 1; Length 273;
Best Local Similarity 82.4%; Pred. No. 7.8e-82;
Matches 225; Conservative 18; Mismatches 30; Indels 0; Gaps 0;

Oy 1 MKKTQWILNTICIVQLLLFNPLVTSEIGCRNRVNNVAVDTKLVAANLPKDYMITLKRVPG 60
1 MKKTQWILNTICIVQLLLFNPLVTQGI CRNPYIDNKKDIKLVAANLEPNDMITLVNYAG 60
Db 1 MKKTQWILNTICIVQLLLFNPLVTQGI CRNPYIDNKKDIKLVAANLEPNDMITLVNYAG 60

Oy 61 MDVLPSHCWISENVVGLSDSTLTDLDDKFSNISSEGLSNYSIIDKLVNIVDDLVECVKENSS 120
Db 61 MDVLPSHCWLRNDWTHLSVSLTLTLDKFSNISSEGSLSNYSIIDKLGKIVDDIVACMEENAP 120

Oy 121 KDKLKSRSPEPRPLFTGEEEFRRINERSIDAFKPDVVVASSEISDCVSSSTLSPKDSRYSVT 180
121 KNVESLSKPEPTRNFTEEBEFPISFRNSIDAEPKPMVASDTSDCVLSSTLGPEDKSRVSVT 180

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QY 181 KPFPMPVAAASSLRNDSSSSNRKAKNPPGDDSLHMAAMLPALFSLIIGFAGALYMKR 240
 DB 181 KPFPMPVAAASSLRNDSSSSNRKAKSPEDPGIQTWATMLPALISLIVGAFGALYMKK 240
 QY 241 QPSLTRAVENIQINEDNEISMLQEKEREFQEV 273
 DB 241 QPSLTRAVENIQINEDNEISMLQEKEREFQEV 273
 RESULT 10
 SCF_MOUSE STANDARD; PRT; 273 AA.
 ID SCF_MOUSE
 AC F20826; P97332; Q62524; Q64222; Q921N5;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE kit ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast cell growth factor) (MGF) (hematopoietic growth factor KL) (Steel factor).
 GN KITLG OR KITL OR MGF OR SL OR SLF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN 11
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=MCB6F1;
 RX MEDLINE=91004223; PubMed=1698558;
 RA Anderson D.M., Lyman S.D., Baird A., Wignall J.M., Bisenman J., Rauch C., March C.J., Boswell H.S., Gimpel S.D., Cosman D., Williams D.E.;
 RT "Molecular cloning of mast cell growth factor, a hematopoietin that is active in both membrane bound and soluble forms.";
 RL Cell 63:1235-243 (1990).
 RN 12
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=92330001; PubMed=1378327;
 RA Huang E.J., Nocka K.H., Buck J., Besmer P.;
 RT "Differential expression and processing of two cell associated forms of the kit-ligand: KL-1 and KL-2";
 RL Mol. Biol. Cell 3:349-362 (1992).
 RN 13
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=MCB6F1;
 RX MEDLINE=91160046; PubMed=1705866;
 RA Flanagan J.G., Chan D.C., Leder P.;
 RT "Transmembrane form of the kit ligand growth factor is determined by alternative splicing and is missing in the Slid mutant.";
 RL Cell 64:1025-1035 (1991).
 RN 14
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=93012940; PubMed=1383087;
 RA Brannan C.I., Bedell M.A., Resnick J.L., Eppig J.J., Handel M.A., Williams D.E., Lyman S.D., Donovan P.J., Jenkins N.A., Copeland N.G.;
 RT "Developmental abnormalities in Steel^{17H} mice result from a splicing defect in the steel factor cytoplasmic tail.";
 RL Genes Dev. 6:1832-1842 (1992).
 RN 15
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J;
 RX MEDLINE=97002551; PubMed=8849898;
 RA Bedell M.A., Copeland N.G., Jenkins N.A.;
 RT "Multiple pathways for steel regulation suggested by genomic and sequence analysis of the murine steel gene.";
 RL Genetics 142:927-934 (1996).
 RN 16
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS PRO-193 AND SER-207.
 RC STRAIN=C3H/EL; TISSUE=Brain;
 RX MEDLINE=97032554; PubMed=8875893;
 RA Graw J., Loester J., Neuhäuser-Klaus A., Pretsch W., Schmitt-John T.;
 RT "Molecular analysis of two new Steel mutations in mice shows a

RT transversion or an insertion.";
 RL Mamm. Genome 7:843-846 (1996).
 RN 17
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS SER-122; PRO-193 AND SER-207.
 RC STRAIN=102/El x C3H/El;
 RX MEDLINE=98025115; PubMed=9360640;
 RA Graw J., Neuhäuser-Klaus A., Pretsch W.;
 RT "Detection of a point mutation (A to G) in exon 5 of the murine Mgf gene defines a novel allele at the Steel locus with a weak phenotype.";
 RL Mutat. Res. 382:75-78 (1997).
 RN 18
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi U., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuenl P., Lewis S., Matsuo Y., Nikaio I., Pesole G., Quackenbush J., Schriml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombert P., Norioka P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L., Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S., Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN 19
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT SER-207.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W., Vialalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Bladesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E., Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN 110
 RP SEQUENCE OF 1-270 FROM N.A. (ISOFORM 1), AND SEQUENCE OF 26-65.
 RX MEDLINE=91004221; PubMed=1698557;
 RA Huang E., Nocka K., Beier D.R., Chu T.Y., Buck J., Lahm H.W., Wellner D., Leder P., Besmer P.;
 RT "The hematopoietic growth factor KL is encoded by the Sl locus and is the ligand of the c-kit receptor, the gene product of the W locus.";
 RL Cell 63:225-233 (1990).
 RN 111
 RP SEQUENCE OF 1-201 FROM N.A.
 RX MEDLINE=91004220; PubMed=1698556;
 RA Zeebo K.M., Williams D.A., Geisler E.N., Broudy V.C., Martin F.H., Atkins H.L., Hsu R.-Y., Birkett N.C., Okino K.H., Mudrock D.C., Jacobsen F.W., Langley K.E., Smith K.A., Takeishi T., Cattaneach B.M.,

RA Galli S.J., Suggs S.V.;
 RT "stem cell factor is encoded at the sl locus of the mouse and is the
 RT ligand for the c-kit tyrosine kinase receptor.";
 RL Cell 63:213-224(1990).
 RN [12]
 RP SEQUENCE OF 26-53.
 RX MEDLINE=91004216; PubMed=1698554;
 RA Copeland N.G., Gilbert D.J., Cho B.C., Donovan P.J., Jenkins N.A.,
 RA Cosman D., Anderson D., Lyman S.D., Williams D.E.;
 RT "Mast cell growth factor maps near the steel locus on mouse
 RT chromosome 10 and is deleted in a number of steel alleles.";
 RL Cell 63:175-183(1990).
 RN [13]
 RP PARTIAL SEQUENCE OF 26-78.
 RX MEDLINE=91004215; PubMed=1698553;
 RA Williams D.E., Eisenman J., Baird A., Rauch C., van Nese K.,
 RA March C.J., Park L.S., Martin U., Nockhizuki D.Y., Boswell H.S.,
 RA Burgess G.S., Cosman D., Lyman S.D.;
 RT "Identification of a ligand for the c-kit proto-oncogene.";
 RL Cell 63:167-174(1990).
 CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
 CC augment the proliferation of both myeloid and lymphoid
 CC hematopoietic progenitors in bone marrow culture. Mediates also
 CC cell-cell adhesion. Acts synergistically with other cytokines,
 CC probably interleukins.
 CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
 CC Also exists as a secreted soluble form (isoform 1 only) (by
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=KL-1;
 CC Name=2; Synonyms=KL-2;
 CC IsoId=P20826-1; Sequence=displayed;
 CC IsoId=P20826-2; Sequence=VSP_006023;
 CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -1- PTM: A soluble form is produced by proteolytic processing of
 CC isoform 1 in the extracellular domain.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC -----
 DR EMBL; M59915; AAA40095.1; -;
 DR EMBL; M57647; AAA39538.1; -;
 DR EMBL; S40534; AAB22555.2; -;
 DR EMBL; X69989; CAA48778.1; -;
 DR EMBL; U44724; -; NOT ANNOTATED_CDS.
 DR EMBL; U44725; AAC52447.1; -;
 DR EMBL; X95381; CAA64667.1; -;
 DR EMBL; X99322; CAA67698.1; -;
 DR EMBL; Y10287; CAA71329.1; -;
 DR EMBL; AK018777; BAB31402.1; -;
 DR EMBL; BC011322; AAA11322.1; -;
 DR EMBL; S40364; AAB22554.2; -;
 DR EMBL; M59912; AAA39539.1; -;
 DR PIR; A37934; A37934.
 DR PIR; S65801; S65801.
 DR MGD; MGI:96974; Kiti1.
 DR GO; GO:0016021; C:integral to membrane; IDA.
 Query March 82.8%; Score 1157; DB 1; Length 273;
 Best Local Similarity 82.8%; Pred. No. 9.3e-82;
 Matches 226; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 1 MKKTQWITLCIYVQLLEFNPVLTGECIRNRVNNVADYTKLVANLPKDMITLTKVPV 60
 DB 1 MKKTQWITLCIYVQLLEFNPVLTGECIRNRVNNVADYTKLVANLPKDMITLTKVPV 60

QY 61 MDVPSHCWISWVYQLSDLTDLDFKFSNISEGLSNYSIIDKLVNIYDDLVECVKENS 120
 DB 61 MDVPSHCWLRDMVYQLSLSTLTLDKFSNISEGLSNYSIIDKLVNIYDDLVECVKENS 120
 QY 121 KDLKSPKSPPEPRLFTPEEFRIENRSIDAFKDPVVASETDCCVVSSTLSPKDSRVST 180
 DB 121 KNIKSPKRPFRSTPEEFPSIFNRSIDAFKDPVVASETDCCVVSSTLSPKDSRVST 180
 QY 181 KPFMLPVAASSLRNDSSSNKAKNPGRDSSLHMAANLPLPFLIIGFAGALYMKR 240
 DB 181 KPFMLPVAASSLRNDSSSNKAKNPGRDSSLHMAANLPLPFLIIGFAGALYMKR 240
 QY 241 OPSLRAVENIQINEEDNISMLQEKREFOEV 273
 DB 241 QSSLRAVENIQINEEDNISMLQEKREFOEV 273

RESULT 11
 SCF SHEEP
 ID - SCF SHEEP STANDARD; PRT; 267 AA.
 AC P79368; Q28591.
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Kit ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast
 DE cell growth factor) (MGP) (fragment).
 GN KITLG OR SCF.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Caprinae; Ovis.
 OC NCBI_TaxId=9940;
 RN [1]
 RP SEQUENCE OF 8-267 FROM N.A.
 RX TISSUE=ovarian follicle;
 RX MEDLINE=96413880; PubMed=8662240;
 RT Tisdall D.J., Quirke L.D., Galloway S.M.;
 RT "Ovine stem cell factor gene is located within a syntenic group on
 RT chromosome 3 conserved across mammalian species.";
 RL Mamm. Genome 7:472-473(1996).
 RN [2]
 RP SEQUENCE OF 1-202 FROM N.A.
 RA McInnes C.J., Logan M., Falconer V.M., Rawlins P., Huntly J., Haig D.;
 RT "Molecular cloning and biological activity of ovine stem cell
 RT factor.";
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
 CC augment the proliferation of both myeloid and lymphoid
 CC hematopoietic progenitors in bone marrow culture. Mediates also
 CC cell-cell adhesion. Acts synergistically with other cytokines,
 CC probably interleukins (by similarity).
 CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
 CC secreted soluble form (by similarity).
 CC -1- PTM: A soluble form is produced by proteolytic processing of
 CC the extracellular domain (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC -----
 DR EMBL; U98974; AAB69491.1; -;
 DR EMBL; Z50743; CAA90620.1; -;
 DR PIR; S58313; S58313.
 DR InterPro; IPR003452; SCF.
 DR Pfam; PF02404; SCF_1.
 KM Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.


```
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 >267 KIT LIGAND.
FT DOMAIN 26 215 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 216 238 POTENTIAL.
FT DOMAIN 239 >267 CYTOPLASMIC (POTENTIAL).
FT DISULFID 29 114 BY SIMILARITY.
FT DISULFID 68 164 BY SIMILARITY.
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 267 267
SQ SEQUENCE 267 AA; 30148 MW; 909095949BEC41 CRC64;

Query Match 82.8%; Score 1156.5; DB 1; Length 267;
Best Local Similarity 85.0%; Pred. No. 9,9e-82;
Matches 227; Conservative 19; Mismatches 20; Indels 1; Gaps 1;

QY 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNVKDTKLVANLPKDYMTTLKYVPG 60
1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNVKDTKLVANLPKDYMTTLKYVPG 60
DB 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNVKDTKLVANLPKDYMTTLKYVPG 60
QY 61 MDVLPBHCWISSEWVQSDSLTDLDFKFSNISGLSNYSIIDKLVNIYDDLYECVKENS 120
61 MDVLPBHCWISSEWVQSDSLTDLDFKFSNISGLSNYSIIDKLVNIYDDLYECVKENS 120
DB 61 MDVLPBHCWISSEWVQSDSLTDLDFKFSNISGLSNYSIIDKLVNIYDDLYECVKENS 120
QY 121 KDLKSKFSPERPLFTPEEFRIENRSDAFKDF-VVASETSDCVVSTLSPEKDSRVAV 179
121 KDLKSKFSPERPLFTPEEFRIENRSDAFKDF-VVASETSDCVVSTLSPEKDSRVAV 179
DB 121 ENVKSKSPERPLFTPEEFRIENRSDAFKDF-VVASETSDCVVSTLSPEKDSRVAV 180
QY 180 TKRPMPLPVAASSLRNDSSSNRKANPPGDSLSHMAAMALPALFSLIIGFAFGALYMK 239
180 TKRPMPLPVAASSLRNDSSSNRKANPPGDSLSHMAAMALPALFSLIIGFAFGALYMK 239
DB 181 TKRPMPLPVAASSLRNDSSSNRKANPPGDSLSHMAAMALPALFSLIIGFAFGALYMK 240
QY 240 RQPSLTRAVENIOINEEDNEISMLOER 266
240 RQPSLTRAVENIOINEEDNEISMLOER 266
DB 241 KQPLTRVENVQINEEDNEISMLOER 267

RESULT 12
SCF_CHICK
ID SCF_CHICK STANDARD; PRT; 287 AA.
AC 009108;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
DE cell growth factor) (MGP).
GN KITLG OR SCF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OK NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93273244; PubMed=7684722;
RA Zhou J., Ohtaki M., Sakurai M.;
RT "Sequence of a cDNA encoding chicken stem cell factor.";
RL Gene 127:269-270(1993).
CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
CC augment the proliferation of both myeloid and lymphoid
CC hemopoietic progenitors in bone marrow culture. Mediates also
CC cell-cell adhesion. Acts synergistically with other cytokines,
CC probably interleukins (By similarity).
CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
CC secreted soluble form (By similarity).
CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC -1- PTM: A soluble form is produced by proteolytic processing of
CC the extracellular domain (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC
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CC -----
DR EMBL, D13516; BAA02733.1; -.
DR PIR, J06037; J06037.
DR InterPro, IPR003452; SCF.
DR Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
KW P1am; PF02404; SCF; 1.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 287 KIT LIGAND.
FT DOMAIN 26 225 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 226 246 POTENTIAL.
FT DOMAIN 247 287 CYTOPLASMIC (POTENTIAL).
FT DISULFID 29 117 BY SIMILARITY.
FT DISULFID 68 167 BY SIMILARITY.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 287 AA; 32328 MW; 6A85556ADC152578 CRC64;

Query Match 50.3%; Score 703; DB 1; Length 287;
Best Local Similarity 51.9%; Pred. No. 6,4e-47;
Matches 149; Conservative 50; Mismatches 74; Indels 14; Gaps 6;

QY 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNVKDTKLVANLPKDYMTTLKYVPG 60
1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNVKDTKLVANLPKDYMTTLKYVPG 60
DB 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNVKDTKLVANLPKDYMTTLKYVPG 60
QY 61 MDVLPBHCWISSEWVQSDSLTDLDFKFSNISGLSNYSIIDKLVNIYDDLYECVKEN 117
61 MDVLPBHCWISSEWVQSDSLTDLDFKFSNISGLSNYSIIDKLVNIYDDLYECVKEN 117
DB 61 MDVLPBHCWISSEWVQSDSLTDLDFKFSNISGLSNYSIIDKLVNIYDDLYECVKEN 120
QY 118 NSSKD-LKSKFSPERPLFTPEEFRIENRSDAFKDFVVASETSDCVVSTLSPEKDS 175
121 DKNDFPIENGHVLEEDFIPENFRLNFTIYKKEADSLDNDCTMPTVETPEKDS 180
DB 121 DKNDFPIENGHVLEEDFIPENFRLNFTIYKKEADSLDNDCTMPTVETPEKDS 180
QY 176 RVSVTKRPMPLPVAASSLRNDSSSNRKANPPGDSLSHMAAMALPALFSLIIG 229
176 RVSVTKRPMPLPVAASSLRNDSSSNRKANPPGDSLSHMAAMALPALFSLIIG 229
DB 181 RVALTKTISFPVAASSLRNDSSSNRKANPPGDSLSHMAAMALPALFSLIIG 240
QY 220 FAFGLYMKRQP-SLTRAVENIOIN--EENNEISMLOERPEQEV 273
241 FILGAIYWKTHPKSPRESNETIOCHGQEEENISMLOERKEHLQV 287

RESULT 13
SCF_COTUA
ID SCF_COTUA STANDARD; PRT; 287 AA.
AC 090314; Q90315;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
DE cell growth factor) (MGP).
GN KITLG OR SCF.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OK NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=96283808; PubMed=8679698;
RA Petite J.N., Kulik M.J.;
RT "Cloning and characterization of cDNAs encoding two forms of avian
RT stem cell factor.";
RL Biochim. Biophys. Acta 1307:149-151(1996).
CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
```



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CC augment the proliferation of both myeloid and lymphoid
CC hematopoietic progenitors in bone marrow culture. Mediates also
CC cell-cell adhesion. Acts synergistically with other cytokines,
CC probably interleukins (By similarity).
CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
CC Also exists as a secreted soluble form (isoform 1 only) (By
CC similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q90314-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q90314-2; Sequence=VSP_006026;
CC -1- PTM: A soluble form is produced by proteolytic processing of
CC isoform 1 in the extracellular domain.
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
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-----
DR EMBL; U43078; AAC59933.1; -
DR EMBL; U43079; AAC59934.1; -
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
KW Alternative splicing.
FT SIGNAL 1 25
FT CHAIN 26 287
FT DOMAIN 26 225
FT TRANSMEM 226 246
FT DOMAIN 247 287
FT DISULFID 29 117
FT DISULFID 68 167
FT CARBOHYD 100 100
FT CARBOHYD 106 106
FT CARBOHYD 149 149
FT CARBOHYD 178 178
FT CARBOHYD 200 200
FT CARBOHYD 206 206
FT VARSELIC 179 213
FT FT
FT FT
SQ SEQUENCE 287 AA; 32455 MW; ABA81AER422A702E CRC64;

Query Match 50.3%; Score 702; DB 1; Length 287;
Best Local Similarity 51.6%; Pred. No. 7,7e-47;
Matches 148; Conservative 51; Mismatches 74; Indels 14; Gaps 6;

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RESULT 14
PTP3_DICD1
ID PTP3_DICD1 STANDARD; PRT; 989 AA.
AC P54637;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Protein-tyrosine phosphatase 3 (EC 3.1.3.48) (Protein-tyrosine-
DE phosphate phosphatase 3).
GN (PTPCL OR PTP3) AND (PTPC2 OR PTP3).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_Taxid=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX3;
RX MEDLINE=96189126; PubMed=8628311;
RA Gamper M., Howard P.K., Hunter T., Firtel R.A.;
RT "Multiple roles of the novel protein tyrosine phosphatase PTP3 during
RT Dictyostelium growth and development.";
RL Mol. Cell. Biol. 16:2431-2444 (1996).
CC -1- FUNCTION: SEEMS TO DEPHOSPHORYLATE A PROTEIN OF 130 kDa (P130).
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: IN THE ANTERIOR-LIKE AND PRESTALK CELL TYPES.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT MODERATE LEVELS DURING GROWTH
CC AND DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
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-----
DR EMBL; U318197; AAC47041.1; -
DR HSSP; O06124; 2SHD.
DR DictyDb; DD01111; ptpcl.
DR DictyDb; DP07777; ptpc2.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PFO0102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTVHPHTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolyase.
FT ACT SITE 649 649
FT DOMAIN 460 716
FT DOMAIN 64 71
FT DOMAIN 109 118
FT DOMAIN 137 190
FT DOMAIN 249 257
FT DOMAIN 258 265
FT DOMAIN 286 289
FT DOMAIN 366 371
FT DOMAIN 787 790
FT DOMAIN 834 839
FT DOMAIN 883 892
FT DOMAIN 906 914
FT DOMAIN 943 963
FT FT
FT FT
SQ SEQUENCE 989 AA; 109995 MW; 9371105AF80974AF CRC64;

Query Match 7.7%; Score 107.5; DB 1; Length 989;
Best Local Similarity 19.1%; Pred. No. 1.4;
Matches 45; Conservative 53; Mismatches 81; Indels 57; Gaps 9;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 14:59:08 ; Search time 31.9628 Seconds
(without alignments)

2204.073 Million cell updates/sec

Title: US-09-224-683-61

Sequence: 1 MKKTQWILTCIYLQALLFN.....NEEDNEISMLQEKEREFQEV 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

SPTRMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriapi:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	865	61.9	208	11	Q64384
2	509	36.4	123	11	Q61854
3	480	34.4	160	11	Q8C9K1
4	375	26.8	271	13	Q9YGP2
5	302	21.6	270	13	Q8AAN7
6	145	10.4	36	6	Q8SEF7
7	145	10.4	36	6	Q8SEF7
8	127	9.1	1713	5	Q8MWP2
9	127	9.1	1713	5	Q8MWP2
10	127	9.1	1713	5	Q8MWP2
11	106	7.6	465	16	Q97H56
12	105.5	7.6	1498	3	Q86VK6
13	105.5	7.6	1498	3	Q86VK6
14	102	7.3	792	5	Q9BP03
15	101	7.2	1490	5	Q19545
16	100.5	7.2	402	11	Q35444

17	100.5	7.2	647	10	Q8GSC2	Q8GSC2 oryza sativ
18	100.5	7.2	647	16	Q98PP9	Q98PP9 mycoplasma
19	100	7.2	1501	3	Q96VL9	Q96VL9 botrytis ci
20	99	7.1	937	10	Q9MAL4	Q9MAL4 arabidopsis
21	97.5	7.0	1107	3	Q12271	Q12271 saccharomyc
22	97	6.9	253	11	Q8R546	Q8R546 mus musculus
23	97	6.9	1447	16	Q9PQ08	Q9PQ08 ureaplasma
24	97	6.9	1566	11	Q9R1L5	Q9R1L5 mus musculus
25	96.5	6.9	345	15	Q8QEF1	Q8QEF1 human immun
26	96.5	6.9	373	12	Q8Q528	Q8Q528 chimpanzee
27	96.5	6.9	475	11	Q9D6C8	Q9D6C8 mus musculus
28	96.5	6.9	1056	16	Q8RE77	Q8RE77 fusobacteri
29	96	6.9	464	16	Q8EQ50	Q8EQ50 oceanobacti
30	96	6.9	1185	16	Q8XJP0	Q8XJP0 clostridium
31	96	6.9	3072	12	Q92645	Q92645 clover yell
32	95.5	6.8	345	15	Q8QED8	Q8QED8 human immun
33	95.5	6.8	348	15	Q8QED9	Q8QED9 human immun
34	95.5	6.8	484	5	Q01626	Q01626 caenorhabdi
35	95.5	6.8	614	10	Q91Q29	Q91Q29 arabidopsis
36	95.5	6.8	683	2	Q50281	Q50281 mycoplasma
37	95.5	6.8	806	2	Q9L8P7	Q9L8P7 mycoplasma
38	95.5	6.8	1515	3	Q96VK4	Q96VK4 emericella
39	94.5	6.8	576	11	Q62970	Q62970 ratius norv
40	94.5	6.8	579	11	Q99KW2	Q99KW2 mus musculu
41	94.5	6.8	632	4	Q8NDW9	Q8NDW9 homo sapien
42	94.5	6.8	722	11	Q8BZT8	Q8BZT8 mus musculu
43	94	6.7	550	10	Q48935	Q48935 mentha pipe
44	94	6.7	1896	5	Q8MN73	Q8MN73 dictyosteli
45	93.5	6.7	1816	5	Q81095	Q81095 caenorhabdi

ALIGNMENTS

RESULT 1
Q64384 PRELIMINARY; PRT; 208 AA.
AC Q64384;
DT 01-NOV-1996 (TRMBLrel. 01, Created)
DT 01-NOV-1996 (TRMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TRMBLrel. 22, Last annotation update)
DE Mast cell growth factor (Fragment).
GN KITL OR MGF OR SL OR KL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92330001; PubMed=1378327;
RA Huang E.J., Nocka K.H., Buck J., Besmer P.;
RT "Differential expression and processing of two cell associated forms
of the kit-ligand: KL-1 and KL-2".
RT Mol. Biol. Cell 3:349-362(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91160046; PubMed=1705866;
RA Flanagan J.G., Chan D.C., Leder P.;
RT "Transmembrane form of the kit ligand growth factor is determined by
RT alternative splicing and is missing in the Sid mutant".
RL Cell 64:1025-1035(1991).
DR EMBL; S40536; AAB22556.2; -;
DR EMBL; M64262; AAB39378.1; -;
DR WGD; MG1:96974; Kitl.
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
FT NON TER 208
SQ SEQUENCE 208 AA; 23222 MW; C74DD639566EB817 CRC64;

Query Match 61.9%; Score 865; DB 11; Length 208;
Best Local Similarity 82.8%; Pred. No. 5.8e-63;
Matches 169; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

QY 1 MKKTOTWILTCIYQLLFNPLVKTGICRNRVTNNVKDVTKLVANLPRKDYMITLKYVPG 60
DB 1 MKKTOTWILTCIYQLLFNPLVKTGICRNRVTNNVKDVTKLVANLPRKDYMITLKYVPG 60
QY 61 MDVLPSCWISSENVVOLSLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120
DB 61 MDVLPSCWISSENVVOLSLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120
QY 121 KDLKSKFSPERPLFTPEEFERFENSIDAFKDFVVASSETSDCVSSTLSPKEDSRVSVT 180
DB 121 KDLKSKFSPERPLFTPEEFERFENSIDAFKDFVVASSETSDCVSSTLSPKEDSRVSVT 180
QY 181 KPFLPVAASSLRNDSSSSNRKA 204
DB 181 KPFLPVAASSLRNDSSSSNRKA 204
QY 181 KPFLPVAASSLRNDSSSSNRKA 204
DB 181 KPFLPVAASSLRNDSSSSNRKA 204

RESULT 2
Q61854 PRELIMINARY; PRT; 123 AA.
AC 061854
Q61854
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Mast cell growth factor.
GN KITL OR MGF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97032534; PubMed=8875893;
RA Graw J., Loester J., Neuhäuser-Klaus A., Pretsch W., Schmitt-John T.;
RT "Molecular analysis of two new Steel mutations in mice shows a
transversion or an insertion."
RL Mamm. Genome 7:843-846 (1996).
DR EMBL: X95379; CAA64666.1; -.
DR MGD: MG1:96974; KITL.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF; 1.
SQ SEQUENCE 123 AA; 13892 MW; A872B4554A85D642 CRC64;

Query Match
Best Local Similarity 36.4%; Score 509; DB 11; Length 123;
Matches 98; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKKTOTWILTCIYQLLFNPLVKTGICRNRVTNNVKDVTKLVANLPRKDYMITLKYVPG 60
DB 1 MKKTOTWILTCIYQLLFNPLVKTGICRNRVTNNVKDVTKLVANLPRKDYMITLKYVPG 60
QY 61 MDVLPSCWISSENVVOLSLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120
DB 61 MDVLPSCWISSENVVOLSLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 120
QY 121 K 121
DB 121 K 121

RESULT 3
Q6C9K1 PRELIMINARY; PRT; 160 AA.
AC 06C9K1
Q6C9K1
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Kit ligand (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL: AK041961; BAC31113.1; -.
FT NON TER 160
SQ SEQUENCE 160 AA; 17492 MW; B12AC581346AAE6D CRC64;

Query Match
Best Local Similarity 34.4%; Score 480; DB 11; Length 160;
Matches 92; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 6 TWILTCIYQLLFNPLVKTGICRNRVTNNVKDVTKLVANLPRKDYMITLKYVPGMDVLP 65
DB 46 TWILTCIYQLLFNPLVKTGICRNRVTNNVKDVTKLVANLPRKDYMITLKYVPGMDVLP 105
QY 66 SHCWISSENVVOLSLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 119
DB 106 SHCWISSENVVOLSLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVKENS 159

RESULT 4
Q9YGP2 PRELIMINARY; PRT; 271 AA.
AC Q9YGP2
Q9YGP2
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Steel factor.
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroides; Ambystomatidae;
OC Ambystoma.
OC NCBI_Taxid=8296;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99299573; PubMed=10370116;
RA Parichy D.M., Stigson M., Voss S.R.;
RT "Genetic analysis of steel and the P-G/M/versican-encoding gene AXPg as
candidates for the white (d) pigmentation mutant in the salamander
RT Ambystoma mexicanum."
RL EMBL: AF119044; AAD17253.1; -.
DR EMBL: AF119044; AAD17253.1; -.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF; 1.
SQ SEQUENCE 271 AA; 30075 MW; 876977ABE7D3EB4 CRC64;

Query Match
Best Local Similarity 26.8%; Score 375; DB 13; Length 271;
Matches 100; Conservative 40; Mismatches 111; Indels 26; Gaps 8;

QY 1 MKKTOTWILTCIYQLLFNPLVKTGICRNRVTNNVKDVTKLVANLPRKDYMITLKYVPG 60
DB 1 MKKTOTWILTCIYQLLFNPLVKTGICRNRVTNNVKDVTKLVANLPRKDYMITLKYVPG 60
QY 57 YVPGMDVLPSCWISSENVVOLSLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVK 116
DB 54 YVPGMDVLPSCWISSENVVOLSLSLTDLDKFSNISSEGLSNYSIIDKLVINIVDDLVECVK 110
QY 117 -----ENSSKDLKSKFSPERPLFTPEEFERFENSIDAFKDFVVASSETSDCVS-STLSP 171
DB 111 SOLIDNEBFTIDPFYDGE---FVPEKYEKVTYKTIILFKAIHMDDDSTCELPVTTETP 167
QY 172 EKDSRVSTKPFMLPVAASSLRNDSSSSNRKAKNPDDSSLSHMAAALPLFSLIIGFA 231
DB 168 LSPDIPVGTKPSAKSFSPSSSRKVRREGIPNAKPPSTSG-LALEPPYALISLSLVIGFI 226
QY 232 FGALYMKRQPSLTRAIVE---NIQINEEDNEISMLOE 265

Db 227 IGVCWKMKHRESGCEPTAPCPVRKKAQASMLNQ 263

RESULT 5

Q8ANV7 PRELIMINARY; PRT; 270 AA.

AC Q8ANV7; 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Stem cell factor.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodidae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Katada T., Yamamoto T., Kitano T., Abe S., Kinoshita T.;
 RT "Developmental expression of Xenopus stem cell factor (XSCF).";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB084915; BAC23087.1; -
 SQ SEQUENCE 270 AA; 31017 MW; 462435081000873A CRC64;

Query Match 21.6%; Score 302; DB 13; Length 270;
 Best Local Similarity 29.7%; Pred. No. 8.7e-17;
 Matches 84; Conservative 47; Mismatches 110; Indels 42; Gaps 9;

QY 1 MKKTQWILTCIVYQLLF--NPLVTEGICENRVYNNKDYTKLVANLPKDYMTLTKY 57
 1 MKKTQWILTCIVYQLLF--NPLVTEGICENRVYNNKDYTKLVANLPKDYMTLTKY 53
 Db 58 VPGMDVLPSCWISSENVQVLSLTLDLKFSNISSELSYSITDKLVNIVDLVCKVE 117
 54 VPEKDGLPKHCWLYMVMVETNHLDKLSKFEKNTSQ--NVLIIKQLSWIFGQIRIOCIQ 110
 QY 118 NSSKDLKSKSPKPEPRLPFTPEEPRIFNRSIDAFKDFVVASSESDCVSSTLSPEDSKV 177
 111 NDEMDEPSASLYRVEYIKARDFSVYVSTIEVFKINDTEYSRLCI--LPQEEYEPY 166
 Db 178 SVTKPEML-----PVAASSLRNDSSSNRKAQNPQDSLSHMAALPALFSLI 227
 167 TTEDDDFLIDSNLDLPVPESTRKNKSRPDSARSGETG----TSIQYSTV-LIALACLV 221
 QY 228 IGFAFGAL-YWKKRQPSLTRAVENIQINEEDNEISMLQEKERE 269
 222 IGFLAGVLCIMK-----FKHRTQTQDNLSAVAVEPRAE 255
 Db

RESULT 6

Q8SPM7 PRELIMINARY; PRT; 36 AA.

AC Q8SPM7; 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Mast cell growth factor (Fragment).
 GN MGF.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteheria; Carnivora; Plissipedia; Canidae; Canis.
 NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schmutz S.M., Berryere T.G.;
 RT "MGF sequencing in the dog aids in mapping to CFAL5";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY094360; AAM16279.1; -
 DR InterPro; IPR003452; SCF.
 DR Pfam; PF02404; SCF; 1.
 FT NON_TER 1 1
 FT 36 36

SQ SEQUENCE 36 AA; 4004 MW; D96DD4CF5426F594 CRC64;

Query Match 10.4%; Score 145; DB 6; Length 36;
 Best Local Similarity 78.8%; Pred. No. 4.9e-05;
 Matches 26; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 217 AMALPALSLLIGFAFGALYWKRPQPSLTRAVE 249
 4 SLALPAPFSLVIGFAFGALYWKRPQPSLTRAVE 36
 Db

RESULT 7

Q8IFM4 PRELIMINARY; PRT; 1697 AA.

AC Q8IFM4; 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN PFD1150C.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_TaxID=36329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hamlin N., Pain A., Berriman B., Hall N., Bowman S., Churcher C.,
 RA Harris B., Harris D., Lawson D., Quail M., Barrell B.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL035477; CAD49276.1; -
 SQ SEQUENCE 1697 AA; 203378 MW; 02274728866E0B2A CRC64;

Query Match 9.1%; Score 127; DB 5; Length 1697;
 Best Local Similarity 21.1%; Pred. No. 0.17;
 Matches 53; Conservative 52; Mismatches 102; Indels 44; Gaps 11;

QY 31 NRVYNNVQDVTGLVAN-----LPKDYMTLKYVGM-DVLPSCWISSENV--Q 76
 1201 HKINNNKDTITIVINDNNTLOEQNRITNELONKIKQKNVSDVTTHNINSQILNLSQ 1260
 QY 77 LSDSLTLDLKFSNISSELSN--YSIIDLVNIYD-DLVCKVKNSSKDLKSKSPSEP 132
 1261 AQNSFFNIPMKQINNDINSKRYNVQKITEIINSYDIIN-YNNQNIKDIYQCFKNIQ 1319
 Db 133 KLPTEPEFRIRNRSIDAFKDFVVASSESDCVSSTLSPEDSKRSVTKPEMLPVAASS 192
 1320 QNTTETQNLHKNHKKYFESHQITISIV--KRMQNEKIKIQEFNKKI-----QH 1370
 QY 193 LENDSSSNRKAQNPQDSLSHMAALPAL--FSLIIGFAFGALYWKRPQPSLTRAVE 249
 1371 FKEETQIMINKLIQ--SHIHLHKKLPITQOQLNTIL-----HREOTKMATR 1417
 Db 250 NIQINEEDNEI 260
 1418 SYNMMEEENEM 1428
 QY

RESULT 8

Q8MMP2 PRELIMINARY; PRT; 1711 AA.

AC Q8MMP2; 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Reticulocyte binding protein-like protein 4.
 GN RH4.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Indochina III/CDC;
 MEDLINE=22030722; PubMed=12034462;

RA Kaneko O., Mu J.-B., Tsuboi T., Su X.-Z., Torii M.;
 RT "Gene structure and expression of a Plasmodium falci-parum 220-kDa
 RT protein homologous to the Plasmodium vivax reticulocyte binding
 RL Mol. Biochem. Parasitol. 121:275-278 (2002).
 DR EMBL; AF420309; AAM47174.1; -
 SQ SEQUENCE 1711 AA; 205236 MW; 2548B64576A02A5B CRC64;

Query Match 9.1%; Score 127; DB 5; Length 1711;
 Best Local Similarity 21.1%; Pred. No. 0.17;
 Matches 53; Conservative 52; Mismatches 102; Indels 44; Gaps 11;

QY 31 NRVTVNVKQVTKLVAN-----LPKDYMTLTKYVPGM-DVLPSCMISEMVV---Q 76
 ID Q8MWP1 PRELIMINARY; PRT; 1713 AA.
 AC Q8MWP1;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Reticulocyte binding protein-like protein 4.
 GN RH4.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Honduas I/CDC;
 RX MEDLINE=22030722; PubMed=12034462;
 RA Kaneko O., Mu J.-B., Tsuboi T., Su X.-Z., Torii M.;
 RT "Gene structure and expression of a Plasmodium falciparum 220-kDa
 RT protein homologous to the Plasmodium vivax reticulocyte binding
 RT protein.";
 RL Mol. Biochem. Parasitol. 121:275-278 (2002).
 DR EMBL; AF420310; AAM47175.1; -
 SQ SEQUENCE 1713 AA; 205500 MW; AE975734989F495D CRC64;

QY 1279 AONSFFNIFMFOINNDINSKRYVQKITEIINSYDIIN-YKNKNIDYIOQFNIOQ 1337
 DB 1279 AONSFFNIFMFOINNDINSKRYVQKITEIINSYDIIN-YKNKNIDYIOQFNIOQ 1337
 QY 133 RLFTEPEFRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVSVTKPMLPVAASS 192
 DB 1338 QLTETETOLNHIKONINHFYFESHOTISIV--KMNQNEKLTIOEFNKKI-----QH 1388
 QY 193 LRNDSSSNRKAKNPBGSSSLHWAAMALPAL---FSLIIGFAGALYWKRPQSLTRAWE 249
 DB 1389 FKEETQIMINKLIQP---SHIHLMKMLPTTQOQLNTLIL-----HNEQTKNATR 1435
 QY 250 NIQINEEDNEI 260
 DB 1436 SYNMBEENEM 1446

RESULT 9

QY 31 NRVTVNVKQVTKLVAN-----LPKDYMTLTKYVPGM-DVLPSCMISEMVV---Q 76
 ID Q8MWP1 PRELIMINARY; PRT; 1713 AA.
 AC Q8MWP1;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Reticulocyte binding protein-like protein 4.
 GN RH4.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Honduas I/CDC;
 RX MEDLINE=22030722; PubMed=12034462;
 RA Kaneko O., Mu J.-B., Tsuboi T., Su X.-Z., Torii M.;
 RT "Gene structure and expression of a Plasmodium falciparum 220-kDa
 RT protein homologous to the Plasmodium vivax reticulocyte binding
 RT protein.";
 RL Mol. Biochem. Parasitol. 121:275-278 (2002).
 DR EMBL; AF420310; AAM47175.1; -
 SQ SEQUENCE 1713 AA; 205500 MW; AE975734989F495D CRC64;

Query Match 9.1%; Score 127; DB 5; Length 1713;
 Best Local Similarity 21.1%; Pred. No. 0.18;
 Matches 53; Conservative 52; Mismatches 102; Indels 44; Gaps 11;

QY 31 NRVTVNVKQVTKLVAN-----LPKDYMTLTKYVPGM-DVLPSCMISEMVV---Q 76
 DB 1223 HKINNNLKDIHIVINDNNTLQEQNRINYLQNKIKQIKVSDVFTNINNSQQLINVSQ 1282
 QY 77 LSDSLDLDKFSNISGLSN--YSIIDKLVNIYD--DLVECKENSSKDLKSKFSPEP 132
 DB 1283 AONSFFNIFMFOINNDINSKRYVQKITEIINSYDIIN-YKNKNIDYIOQFNIOQ 1341
 QY 133 RLFTEPEFRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVSVTKPMLPVAASS 192
 DB 1342 QLTETETOLNHIKONINHFYFESHOTISIV--KMNQNEKLTIOEFNKKI-----QH 1392

QY 193 LRNDSSSNRKAKNPBGSSSLHWAAMALPAL---FSLIIGFAGALYWKRPQSLTRAWE 249
 DB 1393 FKEETQIMINKLIQP---SHIHLMKMLPTTQOQLNTLIL-----HNEQTKNATR 1439
 QY 250 NIQINEEDNEI 260
 DB 1440 SYNMBEENEM 1450

RESULT 10

QY 31 NRVTVNVKQVTKLVAN-----LPKDYMTLTKYVPGM-DVLPSCMISEMVV---Q 76
 ID Q8MWP2 PRELIMINARY; PRT; 1716 AA.
 AC Q8MWP2;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Reticulocyte binding protein homolog 4.
 GN RH4.
 OS Plasmodium falciparum (isolate NF54).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_TaxID=5843;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22030722; PubMed=12034462;
 RA Kaneko O., Mu J.-B., Tsuboi T., Su X.-Z., Torii M.;
 RT "Gene structure and expression of a Plasmodium falciparum 220-kDa
 RT protein homologous to the Plasmodium vivax reticulocyte binding
 RT protein.";
 RL Mol. Biochem. Parasitol. 121:275-278 (2002).
 DR EMBL; AF432854; AAM47192.1; -
 SQ SEQUENCE 1716 AA; 205846 MW; 2A3DAC35BEFEF226 CRC64;

Query Match 9.1%; Score 127; DB 5; Length 1716;
 Best Local Similarity 21.1%; Pred. No. 0.18;
 Matches 53; Conservative 52; Mismatches 102; Indels 44; Gaps 11;

QY 31 NRVTVNVKQVTKLVAN-----LPKDYMTLTKYVPGM-DVLPSCMISEMVV---Q 76
 DB 1220 HKINNNLKDIHIVINDNNTLQEQNRINYLQNKIKQIKVSDVFTNINNSQQLINVSQ 1279
 QY 77 LSDSLDLDKFSNISGLSN--YSIIDKLVNIYD--DLVECKENSSKDLKSKFSPEP 132
 DB 1280 AONSFFNIFMFOINNDINSKRYVQKITEIINSYDIIN-YKNKNIDYIOQFNIOQ 1338
 QY 133 RLFTEPEFRIFNRSIDAFKDFVASETSDCVSSTLSPKDSRVSVTKPMLPVAASS 192
 DB 1339 QLTETETOLNHIKONINHFYFESHOTISIV--KMNQNEKLTIOEFNKKI-----QH 1389
 QY 193 LRNDSSSNRKAKNPBGSSSLHWAAMALPAL---FSLIIGFAGALYWKRPQSLTRAWE 249
 DB 1390 FKEETQIMINKLIQP---SHIHLMKMLPTTQOQLNTLIL-----HNEQTKNATR 1436
 QY 250 NIQINEEDNEI 260
 DB 1437 SYNMBEENEM 1447

RESULT 11

QY 31 NRVTVNVKQVTKLVAN-----LPKDYMTLTKYVPGM-DVLPSCMISEMVV---Q 76
 ID Q97H56 PRELIMINARY; PRT; 465 AA.
 AC Q97H56;
 DT 01-OCT-2001 (Tremblrel. 18, Created)
 DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Flagellar hook-length control protein flik.
 GN CAC2157.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VGM B-1787;

RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.,
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium *Clostridium acetobutylicum*."
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL; AE007716; AAK80115.1; -.
 KM Complete proteome.
 SQ SEQUENCE 465 AA; 51441 MW; 076B343B7D0A678B CRC64;

Query Match 7.6%; Score 106; DB 16; Length 465;
 Best Local Similarity 27.5%; Pred. No. 1.8;
 Matches 52; Conservative 35; Mismatches 76; Indels 26; Gaps 8;

QY 38 KDVTKLVANI.PKQYMTLTKVY---PGMDVLPSCWISEMVOLOSLDLDKFSNISE 93
 DB 101 KEIKKIVSKLNGLELDLKDIDKDKTMSLIQO---MLEBMLIKGNACSDDELKAKMKA 157
 QY 94 GLSNYSIIDLKLVNIYVDLVCVENSKDKLKSFKS-----PPRLFTPEFFRINRSI 148
 DB 158 GISD-EVQDKLMKVMHDIKELKNNSGKDLTKTLDLSLSTGNSSLAEKSLIRDI--1 213
 QY 149 DAFKDFVASETSDCVVSTLSPEKDSRVSVTKPFLPVAAASLRN-----DSSSNRK 203
 DB 214 DSLKKKL---NGSDALNSSSKFDNDFEDKGTIDQAGSSVLSNKNKTASYDSDETNEQ 270
 QY 204 AKNPBGDS 212
 DB 271 AKS--GDSS 277

RESULT 12

Q96VK6 PRELIMINARY; PRT; 1498 AA.
 AC Q96VK6;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 GN ABC transporter protein.
 OS *Emeticella nidulans* (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 RN NCBI_TaxID=162425;
 [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=MG096;
 RA Andrade A.C., Braam C., Haas H., De Waard M.A.;
 RT "ABC transporters and resistance to azole fungicides in the ima
 RT mutants of *Aspergillus nidulans*."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL; AJ309280; CAC42216.1; -.
 DR InterPro: IPR003593; AAA ATPase.
 DR InterPro: IPR003439; ABC_transporter.
 DR InterPro: IPR000847; HTH_LYSR.
 DR InterPro: IPR001063; Ribosomal_L22.
 DR Pfam: PF00005; ABC_tran; 2.
 DR ProDom: PD000006; ABC_transporter; 2.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
 DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
 DR PROSITE; PS00464; RIBOSOMAL_L22; 1.
 KM ATP-binding; Transport.
 SQ SEQUENCE 1498 AA; 167675 MW; EBE9FF3FA6110FEB CRC64;

Query Match 7.6%; Score 105.5; DB 3; Length 1498;
 Best Local Similarity 20.3%; Pred. No. 8.5;
 Matches 59; Conservative 41; Mismatches 108; Indels 83; Gaps 10;
 QY 17 LFNPLVKT-----EGICRNRVTNNVQDVTKLVANI.PKQYMTLTK-----YVPG----- 60

DB 263 IMFSAALAPRRLRGVGRKQYAEHMRDY--VMAMLGSHITINTVGNDFIRGVSGGRK 320
 QY 61 -----MDVLPSCWISB-----MVVQSLDSDLTD 83
 DB 321 RVSIAEATLSQAPLQCMNDSTRGDLSANALBFCCKNALMSKYTGSTACVAIYQASQAYD 380
 QY 84 LLDKPSNISSEGLSNY--SIIDKLVNIYVDLVCVENSKDKLKSFKSPEPRLF----- 135
 DB 381 VDKKTVLYEGKQIYFGNTKAKKFFVDMGECPEPRQTTADLTSLTSPAERLYVPGYEG 440
 QY 136 -----TPPEFFRIFRNSIDAFK-----DFVASETSDCVVSTLSPEKDSRVSVTK 181
 DB 441 RVPCPTPEFAAMKRSERAKLMATIEYERQYPIGSPSYAFVADARKAQ--SKRQRVNS 499
 QY 182 PFMLEPVAASSIRNDSSSNRKAKNPBGDSIHHMAMLPALFSILITGFAF 232
 DB 500 PYTI-----SIQOVSLCVVRGFORLRDPSLTSLTIGNFMALLIGSVF 545

RESULT 13

Q9P884 PRELIMINARY; PRT; 1498 AA.
 AC Q9P884;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 GN ABC transporter protein.
 OS *Emeticella nidulans* (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 RN NCBI_TaxID=162425;
 [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=MG096;
 RA Andrade A.C., Van Nistelrooy J.G.M., Haas H., De Waard M.A.;
 RT "ABC transporters and resistance to azole fungicides in the ima
 RT mutants of *Aspergillus nidulans*."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL; AJ276241; CAB76823.1; -.
 DR InterPro: IPR003593; AAA ATPase.
 DR InterPro: IPR003439; ABC_transporter.
 DR InterPro: IPR000847; HTH_LYSR.
 DR InterPro: IPR001063; Ribosomal_L22.
 DR Pfam: PF00005; ABC_tran; 2.
 DR ProDom: PD000006; ABC_transporter; 2.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
 DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
 DR PROSITE; PS00464; RIBOSOMAL_L22; 1.
 KM ATP-binding; Transport.
 SQ SEQUENCE 1498 AA; 167706 MW; AABDEA3FFDIABFEB CRC64;

Query Match 7.6%; Score 105.5; DB 3; Length 1498;
 Best Local Similarity 20.3%; Pred. No. 8.5;
 Matches 59; Conservative 41; Mismatches 108; Indels 83; Gaps 10;

QY 17 LFNPLVKT-----EGICRNRVTNNVQDVTKLVANI.PKQYMTLTK-----YVPG----- 60
 DB 263 IMFSAALAPRRLRGVGRKQYAEHMRDY--VMAMLGSHITINTVGNDFIRGVSGGRK 320
 QY 61 -----MDVLPSCWISB-----MVVQSLDSDLTD 83
 DB 321 RVSIAEATLSQAPLQCMNDSTRGDLSANALBFCCKNALMSKYTGSTACVAIYQASQAYD 380
 QY 84 LLDKPSNISSEGLSNY--SIIDKLVNIYVDLVCVENSKDKLKSFKSPEPRLF----- 135
 DB 381 VDKKTVLYEGKQIYFGNTKAKKFFVDMGECPEPRQTTADLTSLTSPAERLYVPGYEG 440
 QY 136 -----TPPEFFRIFRNSIDAFK-----DFVASETSDCVVSTLSPEKDSRVSVTK 181

Db 441 RVBCTPDEFAAMKRSERAKMAEIEVEROYPIGGSYADAFVARKMQ-SKRORVNS 499
QY 182 PFMLPVAASSLRNDSSSNRKAKNPPGDSLSHMAWALPALPSLIIGFAP 232
Db 500 PYTI-----SINQVSLCVIRGFORLRGDFSLTTTSLIGNFMALIIISVF 545

RESULT 14

Q9BPJ3 PRELIMINARY; PRT; 792 AA.

AC G9BPJ3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Dd kinesin-related protein K2.
GN DDK2.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ax2;
RA Iwai S., Suyama E., Adachi H., Sutoh K.;
RT "Characterization of Kinesin-related Protein K2 from Dictyostelium
discoideum.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ax2;
RX MEDLINE=98359834; PubMed=9693369;
RA De Hostos E.L., McCallfrey G., Sugcang R., Pierce D.W., Vale R.D.;
RT "A Developmentally Regulated Kinesin-related Motor Protein from
Dictyostelium discoideum.";
RN Mol. Biol. Cell 9:2093-2106(1998).
DR EMBL: AB037280; BAB2152.1; -.
DR HSSP: P17119; 3KAR.
DR InterPro: IPR001752; kinesin_motor.
DR Pfam: PF00225; kinesin_1.
DR PRINTS: PRO0380; KINESINHEAVY.
DR SMART: SM00129; KISC: 1.
DR PROSITE: PS50067; KINESIN MOTOR DOMAIN2, 1.
KW ATP-binding; Coiled coil; Microtubules; Motor protein.
SQ SEQUENCE 792 AA; 89360 MW; 023EA2EFD99EB76F CRC64;

Query Match 7.3%; Score 102; DB 5; Length 792;

Best Local Similarity 19.7%; Pred. No. 7.4; Indels 70; Gaps 12;
Matches 59; Conservative 60; Mismatches 111;

QY 13 YQLLLFNPLVKTGEGI-----CNRVTNNVQVTKLVANLPKDY-----MITLKVPGND 62
Db 59 YHQPLLTNTDIDIKLEIESSNNNNPLKNSINNVMQISQUNSHSRALLMQKRNPTN 118
QY 63 VLPSCWISWVQVQLSDSLDLDF-----SNISEGLSNYSIIDKLVNIVDLVECV 115
Db 119 IRPT-----VKKKLDPTKPLTSPNPKPITPISKLNTMNNNNNNNNNNNNNNI 166
QY 116 KENSSKDLKSPSP-EPRLFPEEPFRIFNRSI-----DAKDFVVASFSDCVASSTLS 170
Db 167 NSNNSNSNNNIIISPVQNTTISPN--NLNLSIKFEKSNFTSTMTSSPTTTTSTLN 224
QY 171 PEKDSFVSVTKPEFMLPPVAASSLRNDSSSNRKAKNPPGDSLSHMAWALPALPSLIIG- 229
Db 225 NNNNNNISIS-----SSCSNNSFPDLOQOHALHEMNKIIDQFTQVRGN 268
QY 230 --FARGALYWKRPQSLTRAVENTIQIN---EEBDF-----ISMLOEKEREFQ 272
Db 269 LOSQFNIISEQLKPPRLSISIDIKTRLDPEEKKEVEKIKELKXVLSLKEKEKELME 328

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 168.5 kDa protein.
GN F18C5.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RN None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Fulton L.;
RT "The sequence of C. elegans cosmid F18C5.";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: U29097; AAA68411.1; -.
DR WormPep: F18C5.3; CE02652.
KW Hypothetical protein.
SQ SEQUENCE 1490 AA; 168480 MW; 89FF7AD689A9B668 CRC64;

Query Match 7.2%; Score 101; DB 5; Length 1490;

Best Local Similarity 23.9%; Pred. No. 20;
Matches 58; Conservative 30; Mismatches 89; Indels 66; Gaps 10;

QY 20 NPLVTEGICNRRVTNNVQVTKLVANLPKDYMITLKVPGNDVLPSCWISWVQVQLSD 79
Db 732 NGAVKAE--CPBAKGNRAPEWMOHLGRIVSPAGIQWVLAFFRDVNEH--PSAKVQ-- 784
QY 80 SLTDLDKFSNISSEGLSNYSIID-----KLVNIVDLVECVKENSCKDLKSPFKS 129
Db 785 RVSDDLKSFAG---GLDNESLDHSQLLGYIFKSLTSDIQKLEVERKNGQDKQKGR 841
QY 130 PEPRLFPEEPFRF--FNRSIDAFKDFVVASFSDCVASSTLSPEK---DSRVSVTKP 182
Db 842 PESCLILPAAPQRIQAMSKVIRSRDHVFA--EFFVLLFSSILKEKKEFDLSDSVSRINP 900
QY 183 FM-----LPPVAASSLR-----NDSSSNRKA 204
Db 901 FVKIILDCDFKYEKLISCSMRALSMIQWOLPAIASNSQVSDTLFLILSDYSISIGAG 960
QY 205 KNP 207
Db 961 NKP 963

Search completed: February 5, 2004, 15:07:29
Job time : 32.9628 secs

RESULT 15
ID Q19545
AC Q19545;
PRELIMINARY; PRT; 1490 AA.

PA (AMGE-) AMGEN INC.
 XX Zeebo KM, Suggs SV, Bosselman RA, Martin FH;
 PI WPI, 1995-119233/17.
 XX N-PSDB; AAQ11543.
 DR
 PT New naturally-occurring polypeptide stem cell factor analogues -
 PT have haematopoietic biological activity of stem cell factor and
 PT are used to treat eg leucopenia, AIDS, nerve damage and
 PT infertility
 XX
 XX Disclosure; Fig 44; 127pp; English.
 XX
 CC The SCF has the ability to stimulate growth of primitive
 CC progenitors including early hematopoietic progenitor cells and non-
 CC hematopoietic stem cells such as neural stem cells and primordial
 CC germ stem cells. The product may be used in a pharmaceutical
 CC compen. for treating, in a mammal, leucopenia, thrombocytopenia,
 CC anaemia, AIDS, neoplasia, nerve damage, infertility and
 CC intestinal damage.
 CC See also AAR11708, AAQ11509-Q11543.
 XX
 SQ Sequence 245 AA;
 Query Match 100.0%; Score 1262; DB 12; Length 245;
 Best Local Similarity 100.0%; Pred. No. 1.5e-121;
 Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKTQWTLTLCIYQLLEFNPVKTGICRNRVTNNVADVTKLVAANLPKDYMITLKYYVG 60
 DB 1 MKKTQWTLTLCIYQLLEFNPVKTGICRNRVTNNVADVTKLVAANLPKDYMITLKYYVG 60
 QY 61 MDVLPSCMISEMNVQSDSLTDLKFSNISSEGLSNYSIDKLVINIYVDLVCEKENS 120
 DB 61 MDVLPSCMISEMNVQSDSLTDLKFSNISSEGLSNYSIDKLVINIYVDLVCEKENS 120
 QY 121 KDLKSFSPERPLFTPEEPRIRNRSIDAFKDFVVASETSDCVSSTLSPEKAKNPP 180
 DB 121 KDLKSFSPERPLFTPEEPRIRNRSIDAFKDFVVASETSDCVSSTLSPEKAKNPP 180
 QY 121 KDLKSFSPERPLFTPEEPRIRNRSIDAFKDFVVASETSDCVSSTLSPEKAKNPP 180
 DB 121 KDLKSFSPERPLFTPEEPRIRNRSIDAFKDFVVASETSDCVSSTLSPEKAKNPP 180
 QY 181 GDSLSHMAAMALPALFSLITGFAGALYMKKROPSLTRAVENTIQINEEDNEISMLQEKER 240
 DB 181 GDSLSHMAAMALPALFSLITGFAGALYMKKROPSLTRAVENTIQINEEDNEISMLQEKER 240
 QY 241 EFOEV 245
 DB 241 EFOEV 245
 QY 241 EFOEV 245
 DB 241 EFOEV 245
 RESULT 2
 AAR83979
 ID AAR83979 standard; Protein; 245 AA.
 XX
 AC AAR83979;
 XX
 DT 25-MAR-2003 (updated)
 DT 15-MAY-1996 (first entry)
 XX
 DE Human stem cell factor derived from 5637 bladder carcinoma cell line.
 XX
 KW Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
 KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
 KW transplant; neoplasia; myelosuppression; bone marrow; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT Protein /label= sig_peptide
 FT 26..245
 FT /label= mat_SCF
 XX

PN EP676470-A1.
 XX
 PD 11-OCT-1995.
 XX
 XX 04-OCT-1990; 95EP-0105391.
 PF
 XX 01-OCT-1990; 90US-0589701.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 28-SEP-1990; 90WO-0505548.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 PI Bosselman RA, Martin FH, Suggs SV, Zeebo KM;
 XX WPI, 1995-346090/45.
 DR N-PSDB; AA104891.
 XX
 PT New stem cell factor polypeptide(s) - for stimulating the growth of
 PT primitive progenitor cells, esp. for treating disorders involving
 PT blood cells
 XX
 XX Claim 9; Fig 44; 127pp; English.
 XX
 PS AAR83979 is a human stem cell factor (SCF) derived from the 5637 bladder
 CC carcinoma cell line. Non-naturally occurring SCF and C-terminally
 CC truncated polypeptides, having amino acid sequences sufficiently
 CC duplicative of naturally occurring SCF, stimulate growth of primitive
 CC progenitors such as haematopoietic progenitor cells, neural stem
 CC cells and primordial germ stem cells. The peptides can be used in a
 CC composition for treating leucopenia, anaemia or thrombocytopenia,
 CC for enhancing engraftment of bone marrow during transplantation or
 CC for bone marrow recovery after chemotherapy or radiation-induced bone
 CC marrow aplasia or myelosuppression. They can also be used for
 CC treating neoplasia, nerve damage, infertility, intestinal damage or
 CC myeloproliferative disorders. Antibodies may be raised against the
 CC peptides for use in detection or neutralisation of SCF in serum. SCF
 CC may be useful for the treatment of AIDS and severe combined
 CC immunodeficiency (SCID) states alone or in combination with other
 CC factors such as IL-7.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC
 SQ Sequence 245 AA;
 Query Match 100.0%; Score 1262; DB 16; Length 245;
 Best Local Similarity 100.0%; Pred. No. 1.5e-121;
 Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKTQWTLTLCIYQLLEFNPVKTGICRNRVTNNVADVTKLVAANLPKDYMITLKYYVG 60
 DB 1 MKKTQWTLTLCIYQLLEFNPVKTGICRNRVTNNVADVTKLVAANLPKDYMITLKYYVG 60
 QY 61 MDVLPSCMISEMNVQSDSLTDLKFSNISSEGLSNYSIDKLVINIYVDLVCEKENS 120
 DB 61 MDVLPSCMISEMNVQSDSLTDLKFSNISSEGLSNYSIDKLVINIYVDLVCEKENS 120
 QY 121 KDLKSFSPERPLFTPEEPRIRNRSIDAFKDFVVASETSDCVSSTLSPEKAKNPP 180
 DB 121 KDLKSFSPERPLFTPEEPRIRNRSIDAFKDFVVASETSDCVSSTLSPEKAKNPP 180
 QY 121 KDLKSFSPERPLFTPEEPRIRNRSIDAFKDFVVASETSDCVSSTLSPEKAKNPP 180
 DB 121 KDLKSFSPERPLFTPEEPRIRNRSIDAFKDFVVASETSDCVSSTLSPEKAKNPP 180
 QY 181 GDSLSHMAAMALPALFSLITGFAGALYMKKROPSLTRAVENTIQINEEDNEISMLQEKER 240
 DB 181 GDSLSHMAAMALPALFSLITGFAGALYMKKROPSLTRAVENTIQINEEDNEISMLQEKER 240
 QY 241 EFOEV 245
 DB 241 EFOEV 245
 QY 241 EFOEV 245
 DB 241 EFOEV 245
 RESULT 3
 AAU05267
 ID AAU05267 standard; Protein; 245 AA.

```

XX AC AAU05267;
XX DT 24-OCT-2001 (first entry)
XX DE Human SCF protein isolated from the 5637 bladder carcinoma cell line.
XX KM Human, stem cell factor; SCF; haematopoietic progenitor cell; AIDS;
XX KM blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
XX KM hypopigmentation disorder; viral disorder; 5637 bladder carcinoma.
XX OS Homo sapiens.
XX FH Key
XX FT Protein 1..25
XX FT Protein /label= Signal_peptide
XX FT Protein 26..245
XX FT Protein /label= Mature_SCF
XX PN US6248319-B1.
XX PD 19-JUN-2001.
XX PF 24-MAY-1995; 95US-0449653.
XX PR 10-APR-1991; 91US-0684535.
XX PR 25-NOV-1992; 92US-0982255.
XX PR 16-OCT-1989; 89US-0422383.
XX PR 11-JUN-1990; 90US-0537198.
XX PR 24-AUG-1990; 90US-0573616.
XX PR 01-OCT-1990; 90US-0589701.
XX PR 21-DEC-1993; 93US-0172329.
XX PA (ZSEB/) ZSEBO K M.
XX PA (BOSS/) BOSSELMAN R A.
XX PA (SUGG/) SUGGS S V.
XX PA (MART/) MARTIN F H.
XX PI Zsebo KM, Bosseelman RA, Suggs SV, Martin FH;
XX DR WPI; 2001-407312/43.
XX DR N-PSDB; AAH10462.
XX PT Increasing the number of early haematopoietic progenitor cells in the
XX PT peripheral blood useful for the treatment of blood disorders including
XX PT Hodgkin's disease comprises the administration of human stem cell
XX PT factor -
XX PS Example 3; Fig 44; 210pp; English.
XX CC The present sequence represents human stem cell factor (SCF). The cDNA
XX CC encoding this sequence is isolated from the 5637 bladder carcinoma cell
XX CC line. The sequence is described in an invention relating to novel stem
XX CC cell factors, the polynucleotides encoding them and methods for
XX CC producing the stem cell factors. The methods involve increasing the
XX CC number of early haematopoietic progenitor cells in human peripheral
XX CC blood by administering a haematopoietically effective human stem cell
XX CC factor polypeptide. The methods are useful for the treatment of blood
XX CC disorders, including myelofibrosis, myelocleiosis, osteopetrosis,
XX CC metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's
XX CC disease, lymphoma, Gaucher's disease, Niemann-Pick disease, refractory
XX CC anaemia, malaria, vitamin B12 and folic acid deficiency,
XX CC hypopigmentation disorders i.e. piebaldism and viral induced disorders,
XX CC including AIDS.
XX SQ Sequence 245 AA;
XX
XX Query Match 100.0%; Score 1262; DB 22; Length 245;
XX Best Local Similarity 100.0%; Pred. No. 1,5e-121;
XX Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MKKTQWILTCIYQLLEFNPVTEGICRNRVTNNKVDYKLVANLPKDYMITLKVP 60
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

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DB 1 MKKTQWILTCIYQLLEFNPVTEGICRNRVTNNKVDYKLVANLPKDYMITLKVP 60
QY 61 MDVLPSCWISBEMVQSDSLTDLDFKFSNISEGSSNYSIIDKLVNIYDDIVECKENS 120
DB 61 MDVLPSCWISBEMVQSDSLTDLDFKFSNISEGSSNYSIIDKLVNIYDDIVECKENS 120
QY 121 KDLKKSFKSPBRLFTPEBFRIFNRSIDAFKDFVASTSDCVVSTLSPKGRKNPP 180
DB 121 KDLKKSFKSPBRLFTPEBFRIFNRSIDAFKDFVASTSDCVVSTLSPKGRKNPP 180
QY 181 GSSSLHMAAMALPALPSLIGFAGALYWKROPSLTRAVENTIQINEEDNEISMLOEKER 240
DB 181 GSSSLHMAAMALPALPSLIGFAGALYWKROPSLTRAVENTIQINEEDNEISMLOEKER 240
QY 241 EFOEV 245
DB 241 EFOEV 245

RESULT 4
AAB98368
ID AAB98368 standard; Protein; 245 AA.
XX AC AAB98368;
XX DT 21-AUG-2001 (first entry)
XX DE Human SCF protein sequence SEQ ID NO:63.
XX KM Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
XX KM gene therapy.
XX OS Homo sapiens.
XX PN US6207454-B1.
XX PD 27-MAR-2001.
XX PF 31-DEC-1998; 98US-0224681.
XX PR 21-DEC-1993; 93US-0172329.
XX PR 24-MAY-1995; 95US-0449653.
XX PR 12-JAN-1998; 98US-0005893.
XX PR 25-NOV-1992; 92US-0982255.
XX PR 16-OCT-1989; 89US-0422383.
XX PR 11-JUN-1990; 90US-0537198.
XX PR 24-AUG-1990; 90US-0573616.
XX PR 01-OCT-1990; 90US-0589701.
XX PA (AMGE-) AMGEN INC.
XX PI Zsebo KM, Bosseelman RA, Suggs SV, Martin FH;
XX DR WPI; 2001-36062/38.
XX DR N-PSDB; AAH41345.
XX PT Enhancing efficiency of transfer of polynucleotide into a target
XX PT mammalian cell in vitro, involves exposing cell that expresses a stem
XX PT cell factor receptor to stem cell factor, and introducing a stem
XX PT polynucleotide into cell in vitro -
XX PS Claim 18; Fig 44; 210pp; English.
XX CC The present invention describes a method for enhancing (E) the
XX CC efficiency of transfer of a polynucleotide (I) into a target mammalian
XX CC cell (II) in vitro, comprising exposing (II) that expresses a stem cell
XX CC factor (SCF) receptor to a biologically active SCF, its analogue or
XX CC fragment, which induces cell proliferation, and introducing (I) to (II)
XX CC in vitro. Exposure of SCF to (II) results in increased uptake of (I)
XX CC into the cell. The method is useful for enhancing the efficiency of the
XX CC transfer of a polynucleotide into a target mammalian cell in vitro.
XX CC The method is useful in gene therapy techniques. AAH41301 to AAH41364
XX CC and AAB98351 to AAB98390 represent sequences used in the exemplification

```

CC of the present invention.

XX Sequence 245 AA;

Query Match 100.0%; Score 1262; DB 22; Length 245;

Best Local Similarity 100.0%; Pred. No. 1.5e-121;

Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVQDVKLVANLPKDYMTLTKYVPG 60
 DB 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVQDVKLVANLPKDYMTLTKYVPG 60
 QY 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDLVNIYVDLVECKENSS 120
 QY 121 KDLKSKFSKPEPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSSTLSPKGAKNPP 180
 DB 121 KDLKSKFSKPEPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSSTLSPKGAKNPP 180
 QY 181 GDSSLHMAAMALPALFSLIIGFAGALYMKKROPSLTRAVENIQINEEDNEISMLOEKER 240
 DB 181 GDSSLHMAAMALPALFSLIIGFAGALYMKKROPSLTRAVENIQINEEDNEISMLOEKER 240
 QY 241 EFOEV 245
 DB 241 EFOEV 245

RESULT 5

AAU02461 standard; Protein; 245 AA.

XX AAU02461;

XX 29-AUG-2001 (first entry)

XX Human SCF protein isolated from the 5637 bladder carcinoma cell line.

XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 XX blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 XX anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
 XX 5637 bladder carcinoma.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Protein 1..25 /label= Signal_peptide

XX Protein 26..245 /label= Mature_SCF

XX US6207417-B1.

XX 27-MAR-2001.

XX 07-JUN-1995; 95US-0482918.

XX 21-DEC-1993; 93US-0172329.

XX 16-OCT-1989; 89US-0422383.

XX 11-JUN-1990; 90US-0537198.

XX 24-AUG-1990; 90US-0573616.

XX 01-OCT-1990; 90US-0589701.

XX (ZSEB/) ZSEBO K M.

XX (BOSS/) BOSSELMAN R A.

XX (SUGS/) SUGS S V.

XX (MART/) MARTIN F H.

XX Zsebo KM, Bosseelman RA, Suggs SV, Martin FH;

XX WPI; 2001-298941/31.

XX N-PSDB; AAS04125.

XX Novel nucleic acids encoding stem cell factor useful for treating
 XX disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's
 XX disease, Kala azar, anaemia and septicemia -
 XX Example 5; Fig 44A-44C; 209pp; English.

XX The present sequence representing human SCF (stem cell factor)
 XX protein is isolated from the 5637 bladder carcinoma cell line. The
 XX present invention relates to novel stem cell factors
 XX (AAU02453-AAU02458, AAU02460) and the polynucleotides encoding them.
 XX SCF stimulate primitive progenitor cells including early haematopoietic
 XX progenitor cells. The invention also describes SCF peptides
 XX (AAU02462-AAU02481) and the oligonucleotides (AAS04081-AAS04117) used
 XX in the isolation of human and rat SCF sequences. The polynucleotide
 XX encoding SCF is useful for producing SCF and useful in gene therapy.
 XX It is useful for treating disorders involving blood cells such as
 XX myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
 XX Hodgkin's disease, lymphoma, Gaucher's disease, anaemia, congestive
 XX splenomegaly, Kala azar, sarcoidosis, military tuberculosis, disseminated
 XX fungus disease, Fulminating septicemia, malaria, vitamin B12 and folic
 XX acid deficiency, pyridoxine deficiency, and hypopigmentation disorders
 XX such as piebaldism and vitiligo.

XX Sequence 245 AA;

Query Match 100.0%; Score 1262; DB 22; Length 245;

Best Local Similarity 100.0%; Pred. No. 1.5e-121;

Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVQDVKLVANLPKDYMTLTKYVPG 60
 DB 1 MKKTQWTLTCTIYQLLEFNPVKTGICRNRVTNNVQDVKLVANLPKDYMTLTKYVPG 60
 QY 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDLVNIYVDLVECKENSS 120
 QY 121 KDLKSKFSKPEPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSSTLSPKGAKNPP 180
 DB 121 KDLKSKFSKPEPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSSTLSPKGAKNPP 180
 QY 181 GDSSLHMAAMALPALFSLIIGFAGALYMKKROPSLTRAVENIQINEEDNEISMLOEKER 240
 DB 181 GDSSLHMAAMALPALFSLIIGFAGALYMKKROPSLTRAVENIQINEEDNEISMLOEKER 240
 QY 241 EFOEV 245
 DB 241 EFOEV 245

RESULT 6

AAU02767 standard; Protein; 245 AA.

XX AAU02767;

XX 29-AUG-2001 (first entry)

XX Human SCF protein isolated from the 5637 bladder carcinoma cell line.

XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 XX blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 XX anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
 XX 5637 bladder carcinoma.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Protein 1..25 /label= Signal_peptide

XX Protein 26..245 /label= Mature_SCF

```

XX  US6218148-B1.
PN
XX
XX  17-APR-2001.
PD
XX
XX  21-DEC-1993; 93US-0172329.
PF
XX
XX  25-NOV-1992; 92US-0982255.
PR
XX  16-OCT-1989; 89US-0422383.
PR  11-UTN-1990; 90US-0537198.
PR  24-AUG-1990; 90US-0573616.
PR  01-OCT-1990; 90US-0589701.
XX
XX  (AMGE-) AMGEN INC.
PA
XX
XX  Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
PI  WPI; 2001-281051/29.
DR  N-PSDB; AAS04225.
XX
XX  Isolated DNA sequence, encoding polypeptide product useful for
PT  stimulating growth of early haematopoietic progenitor cells -
XX
XX  Example 5; Fig 44A-44C; 167pp; English.
XX
XX  The present sequence representing human SCF (stem cell factor)
CC  protein is isolated from the 5637 bladder carcinoma cell line. The
CC  present invention relates to novel stem cell factors
CC  (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797) and the polynucleotides
CC  encoding them. SCF stimulate primitive progenitor cells including early
CC  haematopoietic progenitor cells. The invention also describes SCF
CC  peptides (AAU02777-AAU02794) and the oligonucleotides
CC  (AAS04182-AAS04218) used in the isolation of human and rat SCF
CC  sequences. The polynucleotide encoding SCF is useful for producing
CC  SCF and useful in gene therapy. It is useful for treating disorders
CC  involving blood cells such as myelofibrosis, metastatic carcinoma,
CC  acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
CC  Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
CC  sarcoidosis, military tuberculosis, disseminated fungus disease,
CC  fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
CC  pyridoxine deficiency, and hypopigmentation disorders such as
CC  piebaldism and vitiligo.
XX
XX  Sequence 245 AA;
SQ
XX
XX  Query Match 100.0%; Score 1262; DB 22; Length 245;
XX  Best Local Similarity 100.0%; Pred. No. 1.5e-121;
XX  Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 MKKTQWMLTCTIYQLLEFNPVKTGICRNVTNNVKDVTXVANLPKDYMITLTKYVG 60
DB  1 MKKTQWMLTCTIYQLLEFNPVKTGICRNVTNNVKDVTXVANLPKDYMITLTKYVG 60
XX
XX  61 MDVLPSCWISSENVQVSDSLTDLDFKSNISBGLSNYSIIDKLVINVDLVCEKENS 120
QY  61 MDVLPSCWISSENVQVSDSLTDLDFKSNISBGLSNYSIIDKLVINVDLVCEKENS 120
DB  61 MDVLPSCWISSENVQVSDSLTDLDFKSNISBGLSNYSIIDKLVINVDLVCEKENS 120
XX
XX  121 KDILKSPKSPDEPRILFPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKGAKNPP 180
QY  121 KDILKSPKSPDEPRILFPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKGAKNPP 180
DB  121 KDILKSPKSPDEPRILFPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKGAKNPP 180
XX
XX  181 GDSLSLHMAAALPALPSLIIIGFAFALYMKKQPSLTRAVENTQINEEDNEISMLQEKER 240
QY  181 GDSLSLHMAAALPALPSLIIIGFAFALYMKKQPSLTRAVENTQINEEDNEISMLQEKER 240
DB  181 GDSLSLHMAAALPALPSLIIIGFAFALYMKKQPSLTRAVENTQINEEDNEISMLQEKER 240
XX
XX  241 EFOEV 245
QY  241 EFOEV 245
DB  241 EFOEV 245
XX
XX  RESULT 7
XX  AAB73568
ID  AAB73568 standard; Protein; 245 AA.

```

```

XX  AAB73568;
AC
XX
XX  07-AUG-2001 (first entry)
DT
XX
XX  Human SCF protein isolated from the 5637 bladder carcinoma cell line.
DE
XX
XX  Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW  blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW  anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW  5637 bladder carcinoma.
XX
XX  Homo sapiens.
OS
XX
XX  Key Location/Qualifiers
FH  1..25
FT  Protein /label= Signal_peptide
FT  Protein /label= Mature_SCF
XX
XX  US6204363-B1.
PN
XX
XX  20-MAR-2001.
PD
XX
XX  25-NOV-1992; 92US-0982255.
PF
XX
XX  10-APR-1991; 91US-0684535.
PR  16-OCT-1989; 89US-0422383.
PR  11-UTN-1990; 90US-0537198.
PR  24-AUG-1990; 90US-0573616.
PR  01-OCT-1990; 90US-0589701.
XX
XX  (AMGE-) AMGEN INC.
PA
XX
XX  Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
PI  WPI; 2001-256683/26.
DR  N-PSDB; AAB73568.
XX
XX  New stem cell factor polypeptides and their analogs which stimulate
PT  growth of early hematopoietic progenitors, useful for treating aplastic
PT  anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
PT  disease -
XX
XX  Claim 10; Fig 44A-44C; 166pp; English.
XX
XX  The present sequence representing human SCF (stem cell factor)
CC  protein is isolated from the 5637 bladder carcinoma cell line. The
CC  present invention relates to novel stem cell factors
CC  (AAB73561-AAB73568, AAB73571-AAB73576) and the polynucleotides
CC  encoding them. SCF stimulate primitive progenitor cells including early
CC  haematopoietic progenitor cells. The invention also describes SCF
CC  peptides (AAB73578-AAB73597) and the oligonucleotides
CC  (AAH23859-AAH23895) used in the isolation of human and rat SCF
CC  sequences. The polynucleotide encoding SCF is useful for producing
CC  SCF and useful in gene therapy. It is useful for treating disorders
CC  involving blood cells such as myelofibrosis, metastatic carcinoma,
CC  acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
CC  Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
CC  sarcoidosis, military tuberculosis, disseminated fungus disease,
CC  fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
CC  pyridoxine deficiency, and hypopigmentation disorders such as
CC  piebaldism and vitiligo.
XX
XX  Sequence 245 AA;
SQ
XX
XX  Query Match 100.0%; Score 1262; DB 22; Length 245;
XX  Best Local Similarity 100.0%; Pred. No. 1.5e-121;
XX  Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 MKKTQWMLTCTIYQLLEFNPVKTGICRNVTNNVKDVTXVANLPKDYMITLTKYVG 60
DB  1 MKKTQWMLTCTIYQLLEFNPVKTGICRNVTNNVKDVTXVANLPKDYMITLTKYVG 60
XX

```

Oy		61 MDVLSHCWISSMVVOLDSLTDLDLDPKFNISSGSNYSITDKLVNIYVDIVCYCKENS	120
Dd		61 MDVLPSHCWISSEVVOLSDSLTDLDPKFSNISGSLNYSITDKLVNIYVDIVCYCKENS	120
Oy		121 KDLKKSFKSPPEPRLFTPEEPFFRIFNRSIDAFCDFVASSETSDCVSSTLSPKGGAKNP	180
Dd		121 KDLLKSFSPSPERLFTPEEPFFRIFNNSIDAFKDFVASSETSDCVSSTLSPKGGAKNP	180
Oy		181 GDSSLHMAAMALPALFSLIIGFAFGALYYMKRQPSLTRAVENIQINEBNEISMLOEKR	240
Dd		181 GDSLSHMAMALPALFSLIIGFAFGALYYMKRQPSLTRAVENIQINEBNEISMLOEKR	240
Oy		241 EFOEV 245 	
Dd		241 EFOEV 245	
RESULT 8			
XX	ID	AAB96953 standard; Protein; 245 AA.	
AC		AAB96953;	
XX			
DT		13-JUL-2001 (first entry)	
XX			
DE		Human stem cell factor SEQ ID NO: 63.	
XX			
KW		Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;	
KW		gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;	
KW		neurological damage; intestinal damage; infertility; AIDS; SCID;	
XX		severe combined immunodeficiency.	
OS		Homo sapiens.	
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..25	
FT	Protein	/label= signal_peptide	
FT		26..245	
FT		/label= mature_stem_cell_factor	
PN		US6207802-B1.	
PD		27-MAR-2001.	
XX			
Pf		09-NOV-1994; 94US-0336728.	
PR		25-NOV-1992; 92US-0982255.	
PR		16-OCT-1989; 89US-0422383.	
PR		11-JUN-1990; 90US-0537198.	
PR		24-JUN-1990; 90US-0573616.	
PR		01-OCT-1990; 90US-0589701.	
PA		(AMGE-) AMGEN INC.	
PI		Zsebo KM, Bosselman RA, Suggs SV, Martin FH;	
DR		WPl. 2001-353108/37.	
N-PsDB; AAr89105.			
XX			
PT		Noval isolated non-human mammalian stem cell factor polypeptide	
PT		stimulating growth of early haematopoietic progenitor cells, useful for	
PT		treating aplastic anaemia, lymphoma, Letterer-Siwe disease, kala azar,	
sarcoidosis -			
XX			
PS		Example 5; Fig 44; 209pp; English.	
.XX			
CC		The present invention provides the protein and coding sequences of	
CC		mammalian stem cell factors (SCFs). These are capable of stimulating the	
CC		growth of early haematopoietic progenitor cells, neural stem cells and	
CC		primordial germ stem cells. The sequences are useful in the treatment of	
CC		leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal	
CC		nocturnal haemoglobinuria, malaria, pigmentary disorders, neurological	

CC		and intestinal damage; infertility, AIDS and severe combined immunodeficiency (SCID). The present Sequence is an SCF described in the invention.
CC		
CC		
XX		
XX		
SQ	Sequence	245 AA;
	Query Match:	100.0%; Score 1262; DB 22; Length 245;
	Best Local Similarity	100.0%; Pred. No. 1,Se-121;
	Matches 245;	Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY		1 MKKTQTWLTITCIYQLLTFNPLVKEGICRRRVNTNNVDYTKLVANLPKDYMTLKYPG 60 1 MKKTQTWLTITCIYQLLTFNPLVKEGICRRRVNTNNVDYTKLVANLPKDYMTLKYPG 60
Db		
OY		61 MDVLPSHCWISEMVAQSDSLTDLDKFSNISEGLSNYSIIDKLVINIVDDIVECYKENSS 120 ----- 61 MDVLPSHCWISEMVAQSDSLTDLDKFSNISEGLSNYSIIDKLVINIVDDIVECYKENSS 120
Db		
OY		121 KDLKKSPSPRPRLFTPEEPFRINRSIDAQDPVVASSETDCVVSSTLSPKGAKNPP 180 121 KDLKKSPSPRPRLFTPEEPFRINRSIDAQDPVVASSETDCVVSSTLSPKGAKNPP 180
OY		181 GDSSLHNAAMALPALFSLIIGFAFGALYMKRROPSLTRAVENIQINEEDNEISMLQEKER 240 181 GDSSLHNAAMALPALFSLIIGFAFGALYMKRROPSLTRAVENIQINEEDNEISMLQEKER 240
Db		
OY		241 EFOEV 245 241 EFOEV 245
Db		
RESULT 9		
ABG95643		
ID	ABG95643	standard; Protein; 245 AA.
XX		
AC	ABG95643;	
DT		
DT	05-DEC-2002	(first entry)
XX		
DE		Human SCF protein from 5637 bladder carcinoma cell line.
XX		
KM		Stem cell factor; SCF; blood-forming system; blood cell disorder;
KM		haematopoietic system; metastatic carcinoma; acute leukaemia;
KM		multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
KM		refractory erythroblastic anaemia;iliary tuberculosis; cytostatic;
KM		dissminated fungus disease; haematopoietic; tuberculousis;
KM		antianaemic; antifungal; antimalarial; dermatological; human;
KM		5637 Bladder carcinoma cell line.
XX		
OS	Homo sapiens.	
XX		
PX	EP1241258-A2.	
XX		
PD	18-SEP-2002.	
PF		
PF	04-OCT-1990;	2002EP-0008587.
XX		
PR	16-OCT-1989;	89US-0422383.
PR	11-JUN-1980;	90US-0537198.
PR	24-AUG-1990;	90US-0573618.
PR	28-SEP-1990;	90WO-US05548.
PR	01-OCT-1990;	90US-0589701.
PR	04-OCT-1990;	90EP-0310899.
PR	04-OCT-1990;	95EP-0105391.
PA		
PA	(AMGE-) AMGEN INC.	
PI	Zsebo KM,	Sugge SV, Bosselman RA, Martin FH;
XX		
DR	WPI; 2002-684093/74.	
DR	N-PSDB; ABS73860.	
XX		
PT		Production of a human stem cell factor (SCF) polypeptide for treating

PT disorders involving blood cells, such as leukaemia, comprises culturing
PT mammalian cells comprising non-human SCF promoter DNA linked to DNA
PT encoding the human SCF -
XX
XX Example 18; Fig 44; 120pp; English.
XX
CC The present invention relates to novel stem cell factors (SCFs),
CC polynucleotide sequences encoding the SCFs, and methods of producing
CC them. SCFs are involved in the blood-forming (haematopoietic)
CC system in mammals, particularly humans. The method of the invention
CC is useful for the production of human SCF. The stem cell factors are
CC useful to treat disorders involving blood cells e.g. metastatic
CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
CC lymphoma, refractory erythroidleastic anaemia, military tuberculosis,
CC disseminated fungus disease, malaria, and vitiligo. The present
CC sequence represents human SCF protein isolated from the 5637 bladder
CC carcinoma cell line.
XX
SQ Sequence 245 AA;

Query Match 100.0%; Score 1262; DB 23; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.5e-121;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLENPVLTGICRNRVTNNVQVTKLVANLPKDYMTLLKYPG 60
DB 1 MKKTQWILTCIYQLLENPVLTGICRNRVTNNVQVTKLVANLPKDYMTLLKYPG 60
QY 61 MDVLPCHWISSEWVQVSDSLTDLDFKFSNISSELSNYSTIIDKLVINIVDVLVECVENSS 120
DB 61 MDVLPCHWISSEWVQVSDSLTDLDFKFSNISSELSNYSTIIDKLVINIVDVLVECVENSS 120
QY 121 KDILKFSKSPERPLFTPEEFRIFNRSIDAFKDFVASETSDCVVSTLSPEKAKANPP 180
DB 121 KDILKFSKSPERPLFTPEEFRIFNRSIDAFKDFVASETSDCVVSTLSPEKAKANPP 180
QY 181 GDSSLHMAWALPALFSLIIGFAFGALYWKKQPSLTRAVENTIQINEEDNEISMLOEKER 240
DB 181 GDSSLHMAWALPALFSLIIGFAFGALYWKKQPSLTRAVENTIQINEEDNEISMLOEKER 240
QY 241 EFQEV 245
DB 241 EFQEV 245

RESULT 10
AAE22327
ID AAE22327 standard; Protein; 245 AA.
XX
XX AAE22327;
XX AC
XX DT 25-JUL-2002 (first entry)
XX DE
XX Human SCF protein #3.
XX
XX Human; stem cell factor; SCF protein; leucopenia; thrombocytopenia;
XX anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
XX infertility; neoplasia; myelofibrosis; myelocytocytosis; osteoporosis;
XX metastatic carcinoma; acute leukaemia; multiple myeloma; sarcomatosis;
XX Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
XX Letterer-Siwe disease; refractory erythroidleastic anaemia; Kala azar;
XX Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;
XX disseminated fungus disease; Fulminating septicemia; plebaldism; AIDS;
XX acquired immune deficiency syndrome; malaria; military tuberculosis;
XX pyridoxine deficiency; vitamin B12 deficiency; folate acid deficiency;
XX Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Peptide 1..25
XX FT /label= Signal_peptide
XX FT Protein 26..245

PT /note= "Mature human SCF protein"
XX
XX PN US2002018763-A1.
XX
XX 14-FEB-2002.
XX
XX 12-JAN-1998; 98US-0005243.
XX
XX 24-MAY-1995; 95US-0449653.
XX
XX (ZSERB/) ZSERB K M.
XX (BOSS/) BOSSERMAN R A.
XX (SUGG/) SUGGS S V.
XX (MART/) MARTIN F H.
XX
XX Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
XX WPI; 2002-350789/38.
XX
XX N-PSDB; AAD35478.
XX
XX Novel non-naturally-occurring stem cell factor polypeptide, useful for
XX treating leucopenia, thrombocytopenia, anemia and for enhancing
XX engraftment of bone marrow during transplantation in a mammal -
XX
XX Claim 9; Fig 44; 217pp; English.
XX
XX The present invention relates to novel non-naturally-occurring stem cell
XX factor (SCF) polypeptides having an amino acid sequence sufficiently
XX duplicative of that of naturally-occurring SCF to allow possession of
XX haematopoietic biological activity of naturally occurring SCF. Sequences
XX of the invention are useful for treating leucopenia, thrombocytopenia,
XX anaemia and for enhancing bone marrow recovery in treatment of radiation,
XX engraftment of bone marrow during transplantation in mammals and chemical
XX or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
XX are also useful for treating acquired immune deficiency in a human, nerve
XX damage, neoplasia, infertility, myeloproliferative disorder, intestinal
XX damage in a mammal. SCF sequences are useful for preparing biologically
XX active polymer polypeptide adduct, for enhancing transfection of early
XX haematopoietic progenitor cells with a gene, and transfer of a gene into
XX a mammal. They are useful for treating myelofibrosis, myelocytocytosis,
XX osteoporosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
XX Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
XX Letterer-Siwe disease, refractory erythroidleastic anaemia, Di Guglielmo
XX syndrome, congestive splenomegaly, Kala azar, sarcomatosis, primary
XX splenic pancytopenia, disseminated fungus disease, malaria, military
XX tuberculosis, Fulminating septicemia, pyridoxine deficiency, vitamin
XX B12 and folate acid deficiency, Diamond Blackfan anaemia, hypopigmentation
XX disorders such as plebaldism, AIDS (acquired immune deficiency syndrome)
XX and vitiligo. The present sequence is human SCF protein.
XX
XX
SQ Sequence 245 AA;

Query Match 100.0%; Score 1262; DB 23; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.5e-121;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLENPVLTGICRNRVTNNVQVTKLVANLPKDYMTLLKYPG 60
DB 1 MKKTQWILTCIYQLLENPVLTGICRNRVTNNVQVTKLVANLPKDYMTLLKYPG 60
QY 61 MDVLPCHWISSEWVQVSDSLTDLDFKFSNISSELSNYSTIIDKLVINIVDVLVECVENSS 120
DB 61 MDVLPCHWISSEWVQVSDSLTDLDFKFSNISSELSNYSTIIDKLVINIVDVLVECVENSS 120
QY 121 KDILKFSKSPERPLFTPEEFRIFNRSIDAFKDFVASETSDCVVSTLSPEKAKANPP 180
DB 121 KDILKFSKSPERPLFTPEEFRIFNRSIDAFKDFVASETSDCVVSTLSPEKAKANPP 180
QY 181 GDSSLHMAWALPALFSLIIGFAFGALYWKKQPSLTRAVENTIQINEEDNEISMLOEKER 240
DB 181 GDSSLHMAWALPALFSLIIGFAFGALYWKKQPSLTRAVENTIQINEEDNEISMLOEKER 240
QY 241 EFQEV 245
DB 241 EFQEV 245

DB 241 EFOEV 245

RESULT 11

AAV53285

AAV53285 standard; Protein; 246 AA.

27-JUL-2000 (first entry)

Human SCF protein isolated from the 5637 bladder carcinoma cell line.

Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;

primitive progenitor cell; haematopoietic disorder; synergic;

transfection; haematopoietic stem cell; acute blood loss; neoplasia;

cancer.

Homo sapiens.

EP92579-A1.

12-APR-2000.

04-OCT-1990; 99EP-0122861.

16-OCT-1989; 89US-0422383.

11-JUN-1990; 90US-0537198.

24-AUG-1990; 90US-0573616.

28-SEP-1990; 90MO-US05548.

01-OCT-1990; 90US-0589701.

04-OCT-1990; 90EP-0310899.

(AMGE-) AMGEN INC.

Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;

WPI; 2000-259135/23.

N-PSDB; AAA13715.

Production of hematopoietic cells suitable for administration to a

subject using progenitor cells and expanding the cells using stem cell

factor -

Claim 23; Fig 44; 123pp; English.

A method has been developed of making haematopoietic cells suitable for

administration to a subject. The method comprises: (a) obtaining the

haematopoietic progenitor cells from a donor; and (b) expanding the

cells by adding to the cells a haematopoietically effective dose of a

polypeptide product having at least part of the primary structural

confirmation and one or more of the biological properties of naturally

occurring stem cell factor (SCF). The method is useful for stimulating

primitive progenitor cells including early haematopoietic progenitor

cells which are capable of maturing to erythroid, megakaryocyte,

granulocyte, lymphocyte and macrophage cells. SCF results in absolute

increases in haematopoietic cells of both myeloid and lymphoid lineages.

SCF is useful for treating haematopoietic disorders. The method is

useful for expanding early haematopoietic progenitors in synergic,

allogenic or autologous bone marrow transplant. SCF is useful for

enhancing the efficiency of gene therapy based on transfecting

haematopoietic stem cells. SCF is also useful for combating the

myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing

haematopoietic recovery after acute blood loss and as a boost to the

immune system for fighting neoplasia (cancer). The present sequence

represents a specifically claimed human SCF from the present invention.

Sequence 246 AA;

Query Match 99.2%; Score 1251.5; DB 21; Length 246;

Best Local Similarity 99.6%; Pred. No. 1.8e-120;

Matches 245; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKKTO-TWITLCIYQLLFPNLYKTBEICRRRVNNNKDVTYKLVANIPKQWMTLKVP 59

DB 1 MKKTO-TWITLCIYQLLFPNLYKTBEICRRRVNNNKDVTYKLVANIPKQWMTLKVP 60

QY 60 GMDVLPSCWISSEMYVQLSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVECKENS 119

DB 61 GMDVLPSCWISSEMYVQLSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYVDLVECKENS 120

QY 120 SKDLKKSFKSPPEPRLLFTPEEFRIINRSIDAFKDFVVASSETSDCVVSTLSPEKAKNP 179

DB 121 SKDLKKSFKSPPEPRLLFTPEEFRIINRSIDAFKDFVVASSETSDCVVSTLSPEKAKNP 180

QY 180 PDDSSLHMAAMALPALFSLITIGFARGALYMKRQPSLRAVENIOINEDNEISMLQEK 239

DB 181 PDDSSLHMAAMALPALFSLITIGFARGALYMKRQPSLRAVENIOINEDNEISMLQEK 240

QY 240 REFOEV 245

DB 241 REFOEV 246

RESULT 12

AA11711

AA11711 standard; Protein; 273 AA.

20-JUN-1991 (first entry)

Human Stem Cell Factor from HT1080 fibrosarcoma line.

Stem cell factor; SCF; leukopenia; AIDS; haematopoiesis.

Homo sapiens.

Key Location/Qualifiers

Peptide 1..25

Protein 26..273

EP423980-A.

24-APR-1991.

04-OCT-1990; 90EP-0310899.

01-OCT-1990; 90US-0569701.

16-OCT-1989; 89US-0422383.

11-JUN-1990; 90US-0537198.

24-AUG-1990; 90US-0573616.

28-SEP-1990; 90MO-US05548.

(AMGE-) AMGEN INC.

Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;

WPI; 1991-119233/17.

N-PSDB; AAQ11542.

New naturally-occurring polypeptide stem cell factor analogues -

have haematopoietic biological activity of stem cell factor and

are used to treat eg leukopenia, AIDS, nerve damage and

infertility

Disclosure: Fig 42; 127pp; English.

The SCF has the ability to stimulate growth of primitive

progenitors including early hematopoietic progenitor cells and non-

hematopoietic stem cells such as neural stem cells and primordial

germ stem cells. The product may be used in a pharmaceutical

CC compen. for treating, in a mammal, leukopenia, thrombocytopenia,
CC anaemia, AIDS, neoplasia, nerve damage, infertility and
CC intestinal damage.
CC See also AAR11708, AAQ1509-Q11543.
XX

SQ Sequence 273 AA;

Query Match 97.5%; Score 1231; DB 12; Length 273;
Best Local Similarity 89.4%; Pred. No. 2.7e-118;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWIIITCIYLLFNPVLTGICRNRYTNVNDVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWIIITCIYLLFNPVLTGICRNRYTNVNDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPBHCWISENVVQLSDLTDLDFKFSNISGLSNYSIIDKLVNIYVDLVCEKENS 120
DB 61 MDVLPBHCWISENVVQLSDLTDLDFKFSNISGLSNYSIIDKLVNIYVDLVCEKENS 120
QY 121 KDLKKSFKSPBRLFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKG----- 174
DB 121 KDLKKSFKSPBRLFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKDSRVST 180
QY 175 -----KAKNPPGDSLSHMAAMALPALFSLITIGFAGALYMKR 212
DB 181 KPFLPPVAASLSLRDSSSNRKAQPPGDSLSHMAAMALPALFSLITIGFAGALYMKR 240
QY 213 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 245
DB 241 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 273

RESULT 13

AAR20647
ID AAR20647 standard; Protein; 273 AA.

XX AAR20647;
XX
AC 25-MAR-2003 (updated)
DT 30-APR-1992 (first entry)
XX Human mast cell growth factor.
XX
XX hMGF-2.4; hematopoietin; interleukin; IL-3; c-kit oncogene;
XX proliferation.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..25
FT /label= signal
FT Region 26..210
FT /label= extracellular
FT /note= "claimed polypeptide"
FT Region 211..237
FT /label= transmembrane
FT Region 238..273
FT /label= intracellular
XX
XX MO9200376-A.
XX
XX PD 09-JAN-1992.
XX
XX PF 14-JUN-1991; 91WO-US04274.
XX
XX 25-JUN-1990; 90US-0543264.
XX 10-AUG-1990; 90US-0565840.
XX 28-AUG-1990; 90US-0574152.
XX 21-SEP-1990; 90US-0586073.
XX 12-JUN-1991; 91US-0713715.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX

PI Williams DE, Lyman S;
XX
XX MPI; 1992-041558/05.
DR N-PSDB; AAQ20845.
XX

PT New isolated DNA encoding human mast cell growth factor - useful in
PT stimulating proliferation of haematopoietic cells with growth factor,
PT to treat hemolytic and hypoproliferative anaemias
XX
XX Claim 10; Fig 4; 59pp; English.

CC This human MGF has a mature extracellular region of 185 amino acids.
CC There is a second form of hMGF (see AAQ20844) resulting from an
CC alternative mRNA splicing event which deletes an exon encoding an
CC additional 28 amino acids beginning at amino acid 148 of the mature
CC protein. MGF is the ligand for the protein receptor expression product
CC of the c-kit proto-oncogene. MGF can be used to augment the
CC activity of other cytokines. It can influence early lymphoid or
CC myeloid development. See also AAQ20842-3 and AAQ22204-7.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX

SQ Sequence 273 AA;

Query Match 97.5%; Score 1231; DB 13; Length 273;
Best Local Similarity 89.4%; Pred. No. 2.7e-118;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWIIITCIYLLFNPVLTGICRNRYTNVNDVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWIIITCIYLLFNPVLTGICRNRYTNVNDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPBHCWISENVVQLSDLTDLDFKFSNISGLSNYSIIDKLVNIYVDLVCEKENS 120
DB 61 MDVLPBHCWISENVVQLSDLTDLDFKFSNISGLSNYSIIDKLVNIYVDLVCEKENS 120
QY 121 KDLKKSFKSPBRLFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKG----- 174
DB 121 KDLKKSFKSPBRLFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKDSRVST 180
QY 175 -----KAKNPPGDSLSHMAAMALPALFSLITIGFAGALYMKR 212
DB 181 KPFLPPVAASLSLRDSSSNRKAQPPGDSLSHMAAMALPALFSLITIGFAGALYMKR 240
QY 213 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 245
DB 241 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 273

RESULT 14

AAR83978
ID AAR83978 standard; Protein; 273 AA.

XX AAR83978;
XX
AC 25-MAR-2003 (updated)
DT 15-MAY-1996 (first entry)
XX Human stem cell factor derived from HT1080 fibrosarcoma cell line.
XX
XX Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
XX thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
XX transplant; neoplasia; myelosuppression; bone marrow; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..25
FT /label= sig_peptide
FT Protein 26..248
FT /label= mat_SCF
XX
XX EP676470-A1.
XX
XX

PD 11-OCT-1995.
 XX PF 04-OCT-1990; 95SEP-0105391.
 XX PR 01-OCT-1990; 90US-0589701.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-AUG-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 28-SEP-1990; 90MO-US05548.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Rosseiman RA, Martin FH, Suggs SV, Zsebo KM;
 XX WPI; 1995-346090/45.
 DR N-PSDB; AAT04890.
 XX
 PT New stem cell factor polypeptide(s) - for stimulating the growth of
 PT primitive progenitor cells, esp. for treating disorders involving
 PT blood cells
 XX
 PS Claim 9; Fig 42; 127pp; English.
 XX
 CC AAR83978 is a human stem cell factor (SCF) derived from the HT1080
 CC fibrosarcoma cell line. Non-naturally occurring SCF and C-terminally
 CC truncated polypeptides, having amino acid sequences sufficiently
 CC duplicative of naturally occurring SCF, stimulate growth of primitive
 CC progenitors such as haematopoietic progenitor cells, neural stem
 CC cells and primordial germ stem cells. The peptides can be used in a
 CC composition for treating leucopenia, anaemia or thrombocytopenia,
 CC for enhancing engraftment of bone marrow during transplantation or
 CC for bone marrow recovery after chemotherapy or radiation-induced bone
 CC marrow aplasia or myelosuppression. They can also be used for
 CC treating neoplasia, nerve damage, infertility, intestinal damage or
 CC myeloproliferative disorders. Antibodies may be raised against the
 CC peptides for use in detection or neutralisation of SCF in serum. SCF
 CC may be useful for the treatment of AIDS and severe combined
 CC immunodeficiency (SCID) states alone or in combination with other
 CC factors such as IL-7.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC
 CC Sequence 273 AA;
 SQ
 Query Match 97.5%; Score 1231; DB 16; Length 273;
 Best Local Similarity 89.4%; Pred. No. 2.7e-118;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

XX 28-APR-1998 (first entry)
 DT
 XX
 DE Human recombinant stem cell factor protein.
 KW Stem cell factor; SCF; mast cell growth factor; MCGF; Steel factor;
 KW SF; SLF; analogue; treatment; haematopoietic factor; progenitor cell;
 KW pigmentation disorder; haematopoietic disorder.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide Location/Qualifiers
 FT 1..25
 FT /label= leader sequence
 FT Protein 26..274
 FT /note= "mature full length stem cell factor protein"
 XX
 PN W09738101-A1.
 XX
 PD 16-OCT-1997.
 PD
 PF 03-APR-1997; 97MO-US05541.
 PF
 PR 05-APR-1996; 96US-0628428.
 PR
 PA (AMGE-) AMGEN INC.
 PI Lu HS;
 XX WPI; 1997-512718/47.
 DR
 XX
 PT Stem cell factor analogue N10D or N10D/N1D - useful to treat
 PT pigmentation disorder, AIDS, nerve damage, infertility, intestinal
 PT damage or haematopoietic disorder
 XX
 PS Claim 2; Fig 1; 42pp; English.
 XX
 CC This sequence represents a membrane bound form of a human recombinant
 CC stem cell factor (SCF). Stem cell factors are also known as mast cell
 CC growth factors (MCGF) or Steel factors (SF or SLF) are haematopoietic
 CC factors which act on haematopoietic progenitor cells. Analogues of a
 CC wild type SCF sequence have been constructed (see AAW27605 and AAW27606)
 CC which have increased biological activity and stability compared to
 CC unmodified SCF and can be used to treat pigmentation disorders, e.g.
 CC vitiligo, acquired immunodeficiency syndrome, nerve damage, infertility,
 CC intestinal damage or a haematopoietic disorder, e.g. leucopenia,
 CC thrombocytopenia or anaemia, enhance bone marrow engraftment during
 CC transplantation or bone marrow recovery following radiation, chemical or
 CC chemotherapeutic, induced bone marrow aplasia or myelosuppression,
 CC sensitise cells to chemotherapy or mobilise peripheral blood progenitor
 CC cells. It can also be used in an in vitro haematopoietic cell, preferably
 CC bone marrow or peripheral blood progenitor cell, culture medium, where
 CC the cells are optionally subsequently transfected with exogenous DNA.
 CC
 CC Sequence 273 AA;
 SQ
 Query Match 97.5%; Score 1231; DB 18; Length 273;
 Best Local Similarity 89.4%; Pred. No. 2.7e-118;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

Db	181	KPMLPPVAASTLRNDSSSRKAKNPPGDSILHWAMALPALFSLIGFAGALYKKR	240
Qy	213	QPSLTRAVENTIOINEEDNEISMLQEKREFQEV	245
Db	241	QPSLTRAVENTIOINEEDNEISMLQEKREFQEV	273

Search completed: February 5, 2004, 15:05:14
Job time : 35.0964 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 15:03:24 ; Search time 12.8237 Seconds
(without alignments)
808.360 Million cell updates/sec

Title: US-09-224-683-63

Perfect score: 1262
Sequence: 1 MKKTQWILTCIYLQLLFN.....NEEDNISMJQKEREPEV 245

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1262	100.0	245	3	US-08-482-918-63 Sequence 63, Appl
2	1262	100.0	245	3	US-09-224-681-63 Sequence 63, Appl
3	1262	100.0	245	3	US-08-336-728A-63 Sequence 63, Appl
4	1231	97.5	273	1	US-08-220-379B-2 Sequence 2, Appl
5	1231	97.5	273	2	US-08-628-428-9 Sequence 9, Appl
6	1231	97.5	273	3	US-08-482-918-49 Sequence 49, Appl
7	1231	97.5	273	3	US-08-482-918-61 Sequence 61, Appl
8	1231	97.5	273	3	US-09-224-681-49 Sequence 49, Appl
9	1231	97.5	273	3	US-09-224-681-61 Sequence 61, Appl
10	1231	97.5	273	3	US-08-336-728A-48 Sequence 48, Appl
11	1231	97.5	273	3	US-08-336-728A-49 Sequence 49, Appl
12	1231	97.5	273	3	US-08-336-728A-61 Sequence 61, Appl
13	1226	97.1	273	3	US-08-482-918-48 Sequence 48, Appl
14	1226	97.1	273	3	US-09-224-681-48 Sequence 48, Appl
15	1215	96.3	273	3	US-08-482-918-50 Sequence 50, Appl
16	1215	96.3	273	3	US-09-224-681-50 Sequence 50, Appl
17	1212	96.0	273	3	US-08-336-728A-50 Sequence 50, Appl
18	1099	87.1	248	2	US-08-955-848A-82 Sequence 82, Appl
19	1070.5	84.8	266	3	US-08-482-918-57 Sequence 57, Appl
20	1070.5	84.8	266	3	US-09-224-681-57 Sequence 57, Appl
21	1036.5	82.1	274	3	US-08-336-728A-57 Sequence 57, Appl
22	1036.5	82.1	274	3	US-08-336-728A-52 Sequence 52, Appl
23	1020.5	80.9	271	3	US-08-482-918-52 Sequence 52, Appl
24	1020.5	80.9	271	3	US-09-224-681-52 Sequence 52, Appl
25	1014.5	80.4	274	3	US-08-482-918-51 Sequence 51, Appl
26	1014.5	80.4	274	3	US-09-224-681-51 Sequence 51, Appl
27	1014.5	80.4	274	3	US-08-336-728A-51 Sequence 51, Appl

28	1012.5	80.2	274	3	US-08-336-728A-53 Sequence 53, Appl
29	1007	79.8	273	3	US-08-482-918-53 Sequence 53, Appl
30	1007	79.8	273	3	US-09-224-681-53 Sequence 53, Appl
31	992	78.6	273	3	US-08-482-918-42 Sequence 42, Appl
32	992	78.6	273	3	US-09-224-681-42 Sequence 42, Appl
33	992	78.6	273	3	US-08-336-728A-42 Sequence 42, Appl
34	992	78.6	273	3	US-08-336-728A-54 Sequence 54, Appl
35	991	78.5	273	3	US-08-336-728A-54 Sequence 54, Appl
36	991	78.5	273	3	US-08-482-918-55 Sequence 55, Appl
37	991	78.5	273	3	US-09-224-681-55 Sequence 55, Appl
38	991	78.5	273	3	US-08-336-728A-55 Sequence 55, Appl
39	985	78.1	273	3	US-08-482-918-54 Sequence 54, Appl
40	985	78.1	273	3	US-09-224-681-54 Sequence 54, Appl
41	978	77.5	273	1	US-08-341-456A-11 Sequence 11, Appl
42	978	77.5	273	2	US-08-478-414A-11 Sequence 11, Appl
43	978	77.5	273	3	US-08-325-240A-11 Sequence 11, Appl
44	978	77.5	273	3	US-08-898-982-11 Sequence 11, Appl
45	978	77.5	273	4	US-09-371-261-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-482-918-63
Sequence 63, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-63
Query Match 100.0%; Score 1262; DB 3; Length 245;
Best Local Similarity 100.0%; Pred. No 2.6e-125;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKTQWILTCIYLQLLFNPLVKTEGICRNVTNNVQVTKLVANLPKDYMITTKYVG 60
1 MKKTQWILTCIYLQLLFNPLVKTEGICRNVTNNVQVTKLVANLPKDYMITTKYVG 60
Db 1 MKKTQWILTCIYLQLLFNPLVKTEGICRNVTNNVQVTKLVANLPKDYMITTKYVG 60

QY 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIIVDDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIIVDDLVECVKENS 120
QY 121 KDLKKSFKSPPEPRLTPPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGAKNP 180
DB 121 KDLKKSFKSPPEPRLTPPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGAKNP 180
QY 181 GDSLSHMAAMALPALFSLIIGFAGALYMKKROPSLTRAVENIQINEEDNEISMLQEKER 240
DB 181 GDSLSHMAAMALPALFSLIIGFAGALYMKKROPSLTRAVENIQINEEDNEISMLQEKER 240
QY 241 EFOEV 245
DB 241 EFOEV 245

RESULT 2
US-09-224-681-63
Sequence 63, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-63

Query Match 100.0%; Score 1262; DB 3; Length 245;
Best Local Similarity 100.0%; Pred. No. 2.6e-125;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCYIYLLFNPVLYTEGICRRRTNNVADYKLVANLPKDWITLKYPG 60
DB 1 MKKTQWILTCYIYLLFNPVLYTEGICRRRTNNVADYKLVANLPKDWITLKYPG 60
QY 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIIVDDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIIVDDLVECVKENS 120
QY 121 KDLKKSFKSPPEPRLTPPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGAKNP 180
DB 121 KDLKKSFKSPPEPRLTPPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGAKNP 180
QY 181 GDSLSHMAAMALPALFSLIIGFAGALYMKKROPSLTRAVENIQINEEDNEISMLQEKER 240
DB 181 GDSLSHMAAMALPALFSLIIGFAGALYMKKROPSLTRAVENIQINEEDNEISMLQEKER 240
QY 241 EFOEV 245
DB 241 EFOEV 245

RESULT 3
US-08-336-728A-63
Sequence 63, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/537,198
 FILING DATE: 11-JUN-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/422,383
 FILING DATE: 16-OCT-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Clough, David W.
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET NUMBER: 01017/32956
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEFAX: 312/474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 63:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 245 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-336-728A-63

Query Match 100.0%; Score 1262; DB 3; Length 245;
 Best Local Similarity 100.0%; Pred. No. 2 6e-125;
 Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKQTQWILTCIYIQLLEFNPVKTGICRNRVTNNVQVTKLVANLPKDYMTLTKVPG 60
 DB 1 MKQTQWILTCIYIQLLEFNPVKTGICRNRVTNNVQVTKLVANLPKDYMTLTKVPG 60
 QY 61 MDVLPSCWISSEWVQVSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCWISSEWVQVSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGNKPNP 180
 DB 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGNKPNP 180
 QY 181 GDSGLHMAAMALPALFSLIIGFAFALYMKRQPSLTRAVENTIINEEDNEISMLOEKER 240
 DB 181 GDSGLHMAAMALPALFSLIIGFAFALYMKRQPSLTRAVENTIINEEDNEISMLOEKER 240
 QY 241 EFQEV 245
 DB 241 EFQEV 245

RESULT 4

US-08-220-379B-2
 Sequence 2, Application US/08220379B
 Patent No. 5525708
 GENERAL INFORMATION:
 APPLICANT: No. 5525708, Karl
 APPLICANT: Lohell, Robert B
 TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10020
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/220,379B
 FILING DATE: 28-MAR-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr, James F
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: CytoMed/2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-596-9000
 TELEFAX: 212-596-9090
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 273 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: cleavage site
 LOCATION: 164..165
 US-08-220-379B-2

Query Match 97.5%; Score 1231; DB 1; Length 273;
 Best Local Similarity 89.4%; Pred. No. 5.9e-122;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKQTQWILTCIYIQLLEFNPVKTGICRNRVTNNVQVTKLVANLPKDYMTLTKVPG 60
 DB 1 MKQTQWILTCIYIQLLEFNPVKTGICRNRVTNNVQVTKLVANLPKDYMTLTKVPG 60
 QY 61 MDVLPSCWISSEWVQVSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCWISSEWVQVSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGNKPNP 180
 DB 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKGNKPNP 180
 QY 175 -----KXKPPGDSLHMAAMALPALFSLIIGFAFALYMKR 212
 DB 181 KPFLPVAASSLRNDSSSNRAKPNPGDSLHMAAMALPALFSLIIGFAFALYMKR 240
 QY 213 QPSLTRAVENTIINEEDNEISMLOEKERQEV 245
 DB 241 QPSLTRAVENTIINEEDNEISMLOEKERQEV 273

RESULT 5

US-08-628-428-9
 Sequence 9, Application US/08628428
 Patent No. 5885962
 GENERAL INFORMATION:
 APPLICANT: Lu, Hsiang
 TITLE OF INVENTION: SCF ANALOG COMPOSITIONS AND METHODS
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Amgen Inc.
 STREET: 1840 DeHavilland Drive
 CITY: Thousand Oaks
 STATE: CA
 COUNTRY: USA
 ZIP: 91320-1789
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/628,428
 FILING DATE: 05-APR-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Knight, Matthew W
 REGISTRATION NUMBER: 36,846
 REFERENCE/DOCKET NUMBER: A-400
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 273 amino acids

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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..273
OTHER INFORMATION: /note= "NOTE: Mature full length
OTHER INFORMATION: 1-248 SCF protein begins at amino acid 26; amino acid 1-25
OTHER INFORMATION: include Met and leader sequences for membrane band form of hu
US-08-628-428-9

Query Match 97.5%; Score 1231; DB 2; Length 273;
Best Local Similarity 89.4%; Pred. No. 5.9e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLLFNPVLTGECGRNRYNNVADYKLVANPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLLFNPVLTGECGRNRYNNVADYKLVANPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEMVVQSDSLDLDKFSNISSELSNYSIIDKLVNIYVDLVECKENSS 120
DB 61 MDVLPSCWISSEMVVQSDSLDLDKFSNISSELSNYSIIDKLVNIYVDLVECKENSS 120
QY 121 KDLKSKFSPEPRILFTPEEFRIIPNRSIDAFKDFVVASSETSDCVVSTLSPEKSG----- 174
DB 121 KDLKSKFSPEPRILFTPEEFRIIPNRSIDAFKDFVVASSETSDCVVSTLSPEKSGRSVVT 180
QY 175 -----KAKNPQDSSLHMAAMALPALPSLIIGFAFGALYMKR 212
DB 181 KPFLPVAASSLRNDSSSNRKAQNPQDSSLHMAAMALPALPSLIIGFAFGALYMKR 240
QY 213 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 245
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 6

US-08-482-918-49
Sequence 49, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Boeselman, Robert A.
APPLICANT: Sugers, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-49

Query Match 97.5%; Score 1231; DB 3; Length 273;
Best Local Similarity 89.4%; Pred. No. 5.9e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLLFNPVLTGECGRNRYNNVADYKLVANPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLLFNPVLTGECGRNRYNNVADYKLVANPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEMVVQSDSLDLDKFSNISSELSNYSIIDKLVNIYVDLVECKENSS 120
DB 61 MDVLPSCWISSEMVVQSDSLDLDKFSNISSELSNYSIIDKLVNIYVDLVECKENSS 120
QY 121 KDLKSKFSPEPRILFTPEEFRIIPNRSIDAFKDFVVASSETSDCVVSTLSPEKSG----- 174
DB 121 KDLKSKFSPEPRILFTPEEFRIIPNRSIDAFKDFVVASSETSDCVVSTLSPEKSGRSVVT 180
QY 175 -----KAKNPQDSSLHMAAMALPALPSLIIGFAFGALYMKR 212
DB 181 KPFLPVAASSLRNDSSSNRKAQNPQDSSLHMAAMALPALPSLIIGFAFGALYMKR 240
QY 213 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 245
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 7

US-08-482-918-61
Sequence 61, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Boeselman, Robert A.
APPLICANT: Sugers, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid

BEST AVAILABLE COPY

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TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-61

Query Match 97.5%; Score 1231; DB 3; Length 273;
Best Local Similarity 89.4%; Pred. No. 5.9e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVG 60
DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISBGLSNYSIIDKLVINIYVDLVECVENSS 120
DB 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISBGLSNYSIIDKLVINIYVDLVECVENSS 120
QY 121 KDLKSKFSKSPRLFTPEEFRRIFNRSIDAFKDFVVASSTSDCVSSTLSPEKDSRVSVT 180
DB 121 KDLKSKFSKSPRLFTPEEFRRIFNRSIDAFKDFVVASSTSDCVSSTLSPEKDSRVSVT 180
QY 175 -----KAKNPGDSSILHMAAMLPALFSLIIGFAGALYMKR 212
DB 181 KPMPLPVAASSLRNDSSSNRKAKNPQDSSLHMAAMLPALFSLIIGFAGALYMKR 240
QY 213 OPSLTRAVENTIQINEEDNEISMLQEKERFQEV 245
DB 241 OPSLTRAVENTIQINEEDNEISMLQEKERFQEV 273

RESULT 8
US-09-224-681-49
Sequence 49, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/573,616

FILING DATE: 24-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-49

Query Match 97.5%; Score 1231; DB 3; Length 273;
Best Local Similarity 89.4%; Pred. No. 5.9e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVG 60
DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISBGLSNYSIIDKLVINIYVDLVECVENSS 120
DB 61 MDVLPSCWISSEWVQVLSLTDLDKFSNISBGLSNYSIIDKLVINIYVDLVECVENSS 120
QY 121 KDLKSKFSKSPRLFTPEEFRRIFNRSIDAFKDFVVASSTSDCVSSTLSPEKDSRVSVT 180
DB 121 KDLKSKFSKSPRLFTPEEFRRIFNRSIDAFKDFVVASSTSDCVSSTLSPEKDSRVSVT 180
QY 175 -----KAKNPGDSSILHMAAMLPALFSLIIGFAGALYMKR 212
DB 181 KPMPLPVAASSLRNDSSSNRKAKNPQDSSLHMAAMLPALFSLIIGFAGALYMKR 240
QY 213 OPSLTRAVENTIQINEEDNEISMLQEKERFQEV 245
DB 241 OPSLTRAVENTIQINEEDNEISMLQEKERFQEV 273

RESULT 9
US-09-224-681-61
Sequence 61, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-61

Query Match          97.5%; Score 1231; DB 3; Length 273;
Best Local Similarity 89.4%; Pred. No. 5,9e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY      1 MKKTQWILITCIYLQLLFNPVLTKEGICRRNVTNNVDYTKLVANLPRDYMITLKYPG 60
      |||||||
DB      1 MKKTQWILITCIYLQLLFNPVLTKEGICRRNVTNNVDYTKLVANLPRDYMITLKYPG 60
      |||||||

QY      61 MOVLPBHCWISBMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
      |||||||
DB      61 MOVLPBHCWISBMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
      |||||||

QY      121 KOLKSFKSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSVSVT 174
      |||||||
DB      121 KOLKSFKSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSVSVT 180
      |||||||

QY      121 KOLKSFKSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSVSVT 180
      |||||||
DB      121 KOLKSFKSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSVSVT 180
      |||||||

QY      175 -----KAKNP PGDSSLHMAAALPALFSLIIGFAGALYWKRR 212
      |||||||
DB      181 KPFMLPVAASLRNDSSSNRKAKNP PGDSSLHMAAALPALFSLIIGFAGALYWKRR 240
      |||||||

QY      213 QPSLRAVENIQINEDNEISMLQEKREFOEV 245
      |||||||
DB      241 QPSLRAVENIQINEDNEISMLQEKREFOEV 273
      |||||||

RESULT 10
US-08-336-728A-48
; Sequence 48, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
```

```

APPLICANT: Zeebo, Krizztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-48

Query Match          97.5%; Score 1231; DB 3; Length 273;
Best Local Similarity 89.4%; Pred. No. 5,9e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY      1 MKKTQWILITCIYLQLLFNPVLTKEGICRRNVTNNVDYTKLVANLPRDYMITLKYPG 60
      |||||||
DB      1 MKKTQWILITCIYLQLLFNPVLTKEGICRRNVTNNVDYTKLVANLPRDYMITLKYPG 60
      |||||||

QY      61 MOVLPBHCWISBMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
      |||||||
DB      61 MOVLPBHCWISBMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
      |||||||

QY      121 KOLKSFKSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSVSVT 174
      |||||||
DB      121 KOLKSFKSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSVSVT 180
      |||||||

QY      121 KOLKSFKSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSVSVT 180
      |||||||
DB      121 KOLKSFKSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSVSVT 180
      |||||||

QY      175 -----KAKNP PGDSSLHMAAALPALFSLIIGFAGALYWKRR 212
      |||||||
DB      181 KPFMLPVAASLRNDSSSNRKAKNP PGDSSLHMAAALPALFSLIIGFAGALYWKRR 240
      |||||||
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QY      213 QPSLTRAveniQINEEDNEISMLOEKEREFQEV 245
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Db      241 QPSLTRAveniQINEEDNEISMLOEKEREFQEV 273

```

RESULT 11
US-08-336

Sequence 49, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-49

Query Match	97.5%	Score 1231;	DB 3;	Length 273;
Best Local Similarity	89.4%	Pred. NO. 5.9e-122;		
Matches 244; Conservative	0;	Mismatches 1;	Indels 28;	Gaps 1;

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QY 1 MKKTQWMLTCTYQLLLFNPPLYKTGICNNRTNNVKDVTYKIVANIPKQYMITLKVPG 60
    |||||
Db 1 MKKTQWMLTCTYQLLLFNPPLYKTGICNNRTNNVKDVTYKIVANIPKQYMITLKVPG 60
    |||||
QY 61 MDVLPSHCWISLSENVQVLSLTDLLDKFSNISBGLSNYSIIDKLVINIVDDLVECVKENS 120
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D6	61	MDVLPBHCASIKEMVVOQLSDSLTDLIDKSNISIEGLSNYSIIDKLVNIYDDLVECVKENS	122
QY	121	KDLKSKFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVASETSDCVVSTLSPEKG-----	174
D6	121	KDLKSKFKSPPEPRLFTPEEFPRIFNRSIDAFKDFVASETSDCVVSTLSPEKSRVST	180
QY	175	-----KACNPGDSSLIHAAALPALFSLIIGFAGALYKKR	212
D6	181	KPEMLPVAASSLRNDSSSNKAKNPGDSSLIHAAALPALFSLIIGFAGALYKKR	240
QY	213	QPSLTRAIVENIQINEEDNEISMLQEKERFQEV	245
D6	241	QPSLTRAIVENIQINEEDNEISMLQEKERFQEV	273

RESULT 12
US-08-336

Sequence 61, Application US/08336728A
Patent No. 6207802

GENERAL INFORMATION:

APPLICANT: Zsabo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989

ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-336-728A-61

Query Match 97.5%; Score 1231; DB 3; Length 273;
Best Local Similarity 89.4%; Pred. No. 5.9e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYPVG 60
DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYPVG 60
QY 61 MDVLPSCWISPMVQVLSLTDLLDKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120
DB 61 MDVLPSCWISPMVQVLSLTDLLDKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120
QY 121 KDLKSFSPERPLTPPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPEKSG----- 174
DB 121 KDLKSFSPERPLTPPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPEKSGSVST 180
QY 175 -----KAKNPPGDSLHMAAMALPALFSLIIGFAGALYMKR 212
DB 181 KPFMLPVAASLRNDSSSNRKAKNPPGDSLHMAAMALPALFSLIIGFAGALYMKR 240
QY 213 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 245
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 13
US-08-482-918-48
; Sequence 48, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
; APPLICANT: Zeebo, Krizztina M.
; APPLICANT: Bosseiman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-482-918-48

Query Match 97.1%; Score 1226; DB 3; Length 273;
Best Local Similarity 89.0%; Pred. No. 2e-121;
Matches 243; Conservative 0; Mismatches 2; Indels 28; Gaps 1;

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DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYPVG 60
QY 61 MDVLPSCWISPMVQVLSLTDLLDKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120
DB 61 MDVLPSCWISPMVQVLSLTDLLDKFSNISSEGLSNYSIIDKLVNIYDDLVCEKENS 120
QY 121 KDLKSFSPERPLTPPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPEKSG----- 174
DB 121 KDLKSFSPERPLTPPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPEKSGSVST 180
QY 175 -----KAKNPPGDSLHMAAMALPALFSLIIGFAGALYMKR 212
DB 181 KPFMLPVAASLRNDSSSNRKAKNPPGDSLHMAAMALPALFSLIIGFAGALYMKR 240
QY 213 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 245
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 14
US-09-224-681-48
; Sequence 48, Application US/09224681
; Patent No. 6207454
; GENERAL INFORMATION:
; APPLICANT: Zeebo, Krizztina M.
; APPLICANT: Bosseiman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,681
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,893
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:

NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-48

Query Match 97.1%; Score 1226; DB 3; Length 273;
Best Local Similarity 89.0%; Pred. No. 2e-121;
Matches 243; Conservative 0; Mismatches 2; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNKDVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNKDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISEGLSNYSIIDKLVINIYDVLVECVKENS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISEGLSNYSIIDKLVINIYDVLVECVKENS 120
QY 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVAVASSTSDCVVSTLSPEKDSRVST 174
DB 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVAVASSTSDCVVSTLSPEKDSRVST 180
QY 175 -----KAKNPBGDSLSHMAAMLPALFSLITGFAGALYWKRR 212
DB 181 KPEMLPPVAASSLRNDSSSNRKAKNPBGDSLSHMAAMLPALFSLITGFAGALYWKRR 240
QY 213 QPSLTRAIVENIQINEEDNEISMLQEKERFQEV 245
DB 241 QPSLTRAIVENIQINEEDNEISMLQEKERFQEV 273

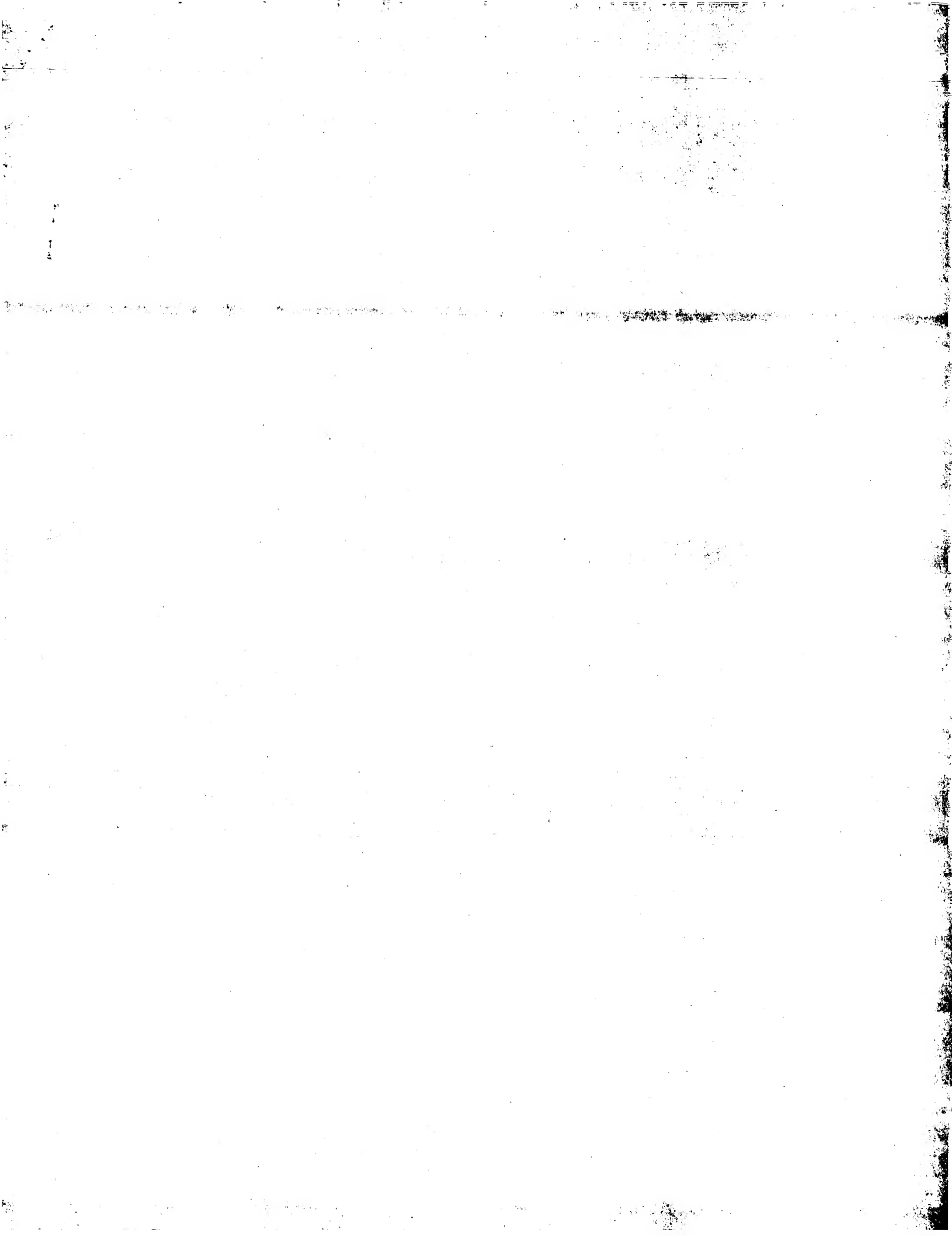
RESULT 15
US-08-482-918-50
Sequence 50, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Garstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-50

Query Match 96.3%; Score 1215; DB 3; Length 273;
Best Local Similarity 88.3%; Pred. No. 2.9e-120;
Matches 241; Conservative 0; Mismatches 4; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNKDVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLFPNPLVTEGICRNRVTNNKDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISEGLSNYSIIDKLVINIYDVLVECVKENS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISEGLSNYSIIDKLVINIYDVLVECVKENS 120
QY 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVAVASSTSDCVVSTLSPEKDSRVST 174
DB 121 KDLKSKSPSPRLFTPEEFRIFNRSIDAFKDFVAVASSTSDCVVSTLSPEKDSRVST 180
QY 175 -----KAKNPBGDSLSHMAAMLPALFSLITGFAGALYWKRR 212
DB 181 KPEMLPPVAASSLRNDSSSNRKAKNPBGDSLSHMAAMLPALFSLITGFAGALYWKRR 240
QY 213 QPSLTRAIVENIQINEEDNEISMLQEKERFQEV 245
DB 241 QPSLTRAIVENIQINEEDNEISMLQEKERFQEV 273

Search completed: February 5, 2004, 15:12:24
Job time: 13.8237 secs



GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 5, 2004, 15:07:35 ; Search time 27.3347 Seconds
(without alignments)
1876.686 Million cell updates/sec

Title: US-09-224-683-63

Perfect score: 1262
Sequence: 1 MKKTQTWILTCIYLQLLFN.....NEEDNEISMLQEXERFQEV 245

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: Published Applications_AA:*
- 2: /cgn2_6/prodata/2/pubppa/US07_PUBCOMB.pep:*
- 3: /cgn2_6/prodata/2/pubppa/PCr_NEW_PUB.pep:*
- 4: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep:*
- 5: /cgn2_6/prodata/2/pubppa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/prodata/2/pubppa/PCrUS_PUBCOMB.pep:*
- 7: /cgn2_6/prodata/2/pubppa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/prodata/2/pubppa/US09_PUBCOMB.pep:*
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- 16: /cgn2_6/prodata/2/pubppa/US10_NEW_PUB.pep:*
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- 18: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1262	100.0	245	US-09-005-243-63	Sequence 63, Appl
2	1262	100.0	245	US-09-224-683-63	Sequence 63, Appl
3	1231	97.5	273	US-09-005-243-49	Sequence 49, Appl
4	1231	97.5	273	US-09-005-243-61	Sequence 61, Appl
5	1231	97.5	273	US-09-224-683-49	Sequence 49, Appl
6	1231	97.5	273	US-09-224-683-61	Sequence 61, Appl
7	1226	97.1	273	US-09-005-243-48	Sequence 48, Appl
8	1226	97.1	273	US-09-224-683-48	Sequence 48, Appl
9	1215	96.3	273	US-09-005-243-50	Sequence 50, Appl
10	1215	96.3	273	US-09-224-683-50	Sequence 50, Appl
11	1070.5	84.8	266	US-09-005-243-57	Sequence 57, Appl
12	1070.5	84.8	266	US-09-224-683-57	Sequence 57, Appl
13	1020.5	80.9	271	US-09-005-243-52	Sequence 52, Appl
14	1020.5	80.9	271	US-09-224-683-52	Sequence 52, Appl
15	1014.5	80.4	274	US-09-005-243-51	Sequence 51, Appl

16	1014.5	80.4	274	US-09-224-683-51	Sequence 51, Appl
17	1007	79.8	273	US-09-005-243-53	Sequence 53, Appl
18	1007	79.8	273	US-09-224-683-53	Sequence 53, Appl
19	992	78.6	273	US-09-005-243-42	Sequence 42, Appl
20	992	78.6	273	US-09-224-683-42	Sequence 42, Appl
21	991	78.5	273	US-09-005-243-55	Sequence 55, Appl
22	991	78.5	273	US-09-224-683-55	Sequence 55, Appl
23	991	78.5	273	US-10-132-345-4	Sequence 4, Appl
24	985	78.1	273	US-09-005-243-54	Sequence 54, Appl
25	985	78.1	273	US-09-224-683-54	Sequence 54, Appl
26	900	71.3	270	US-10-132-345-2	Sequence 2, Appl
27	890	70.5	208	US-09-005-243-46	Sequence 46, Appl
28	890	70.5	208	US-09-224-683-46	Sequence 46, Appl
29	865	68.5	195	US-09-005-243-44	Sequence 44, Appl
30	865	68.5	195	US-09-224-683-44	Sequence 44, Appl
31	758	60.1	164	US-09-903-327A-10	Sequence 10, Appl
32	758	60.1	165	US-10-320-231A-25	Sequence 25, Appl
33	758	60.1	165	US-10-053-355A-2	Sequence 2, Appl
34	758	60.1	166	US-09-748-592-2	Sequence 2, Appl
35	758	60.1	166	US-10-270-555-1	Sequence 1, Appl
36	756	59.9	613	US-09-903-327A-14	Sequence 14, Appl
37	696	55.2	196	US-09-005-243-40	Sequence 40, Appl
38	696	55.2	196	US-09-224-683-40	Sequence 40, Appl
39	594	47.1	165	US-09-005-243-1	Sequence 1, Appl
40	594	47.1	165	US-09-224-683-1	Sequence 1, Appl
41	586	46.4	393	US-10-270-555-2	Sequence 2, Appl
42	564	44.7	282	US-09-005-243-56	Sequence 56, Appl
43	564	44.7	282	US-09-224-683-56	Sequence 56, Appl
44	281	22.3	56	US-10-176-791A-61	Sequence 61, Appl
45	266	21.1	56	US-10-176-791A-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1
US-09-005-243-63
; Sequence 63, Application US/09005243
; Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor.
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-63

Query Match 100.0%; Score 1262; DB 9; Length 245;
Best Local Similarity 100.0%; Pred. No. 5.1e-119;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEPNLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYQLLEPNLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISEGLSNYSIIDKLVNIYVDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISEGLSNYSIIDKLVNIYVDLVECVKENS 120
QY 121 KDLKSFSPKPEPRLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKGAKNPP 180
DB 121 KDLKSFSPKPEPRLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKGAKNPP 180
QY 181 GDSLSHMAAMALPALFSLIIGFAGALYWKROPSLTRAVENIQINEEDNEISMLQEKER 240
DB 181 GDSLSHMAAMALPALFSLIIGFAGALYWKROPSLTRAVENIQINEEDNEISMLQEKER 240
QY 241 EFOEV 245
DB 241 EFOEV 245

RESULT 2

US-09-224-683-63
Sequence 63, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-63

Query Match 100.0%; Score 1262; DB 9; Length 245;
Best Local Similarity 100.0%; Pred. No. 5.1e-119;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEPNLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYQLLEPNLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISEGLSNYSIIDKLVNIYVDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQVSDSLTDLDFKFSNISEGLSNYSIIDKLVNIYVDLVECVKENS 120
QY 121 KDLKSFSPKPEPRLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKGAKNPP 180
DB 121 KDLKSFSPKPEPRLFTPEEFRIFNRSIDAFKDFVASETSDCVSSTLSPKGAKNPP 180
QY 181 GDSLSHMAAMALPALFSLIIGFAGALYWKROPSLTRAVENIQINEEDNEISMLQEKER 240
DB 181 GDSLSHMAAMALPALFSLIIGFAGALYWKROPSLTRAVENIQINEEDNEISMLQEKER 240
QY 241 EFOEV 245
DB 241 EFOEV 245

RESULT 3

US-09-005-243-49
Sequence 49, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.

APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-49

Query Match 97.5%; Score 1231; DB 9; Length 273;
Best Local Similarity 89.4%; Pred. No. 8.1e-116;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWIIITLCITLQILLNPVTKTGICGNRVNKNVQTKVAVLPKDYMTLTKYVVG 60
DB 1 MKKTQWIIITLCITLQILLNPVTKTGICGNRVNKNVQTKVAVLPKDYMTLTKYVVG 60
QY 61 MDVLPSCWISSENVVQSLDLDLDFKSNISSEGLSNYSIIDLVNIIVDLVECVKENS 120
DB 61 MDVLPSCWISSENVVQSLDLDLDFKSNISSEGLSNYSIIDLVNIIVDLVECVKENS 120
QY 121 KDLKSKFKSPRLFTPEEFRRIFNRSIDAFKDFVVAASSTSDCVSSTSPKSG----- 174
DB 121 KDLKSKFKSPRLFTPEEFRRIFNRSIDAFKDFVVAASSTSDCVSSTSPKSKRVSVAT 180

QY 175 -----KANNPPGSSLHWAAVALPALFSLIIGFAGALYMKR 212
DB 181 KPFMPLPVAASSLRRDSSSNRKANNPPGSSLHWAAVALPALFSLIIGFAGALYMKR 240
QY 213 QPSLTRAVENTQINEDNEISMLOKEREPOEV 245
DB 241 QPSLTRAVENTQINEDNEISMLOKEREPOEV 273

RESULT 4
US-09-005-243-61
Sequence 61, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-61

Query Match 97.5%; Score 1231; DB 9; Length 273;
Best Local Similarity 89.4%; Pred. No. 8.1e-116;

Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTOTWILTCIYQLLFNPVLYKTEGICRNRVTNNVQVTKLVANLPKDYMTITLKYPG 60
1 MKKTOTWILTCIYQLLFNPVLYKTEGICRNRVTNNVQVTKLVANLPKDYMTITLKYPG 60
Db 1 MKKTOTWILTCIYQLLFNPVLYKTEGICRNRVTNNVQVTKLVANLPKDYMTITLKYPG 60

QY 61 MDVLPSCWISBMVQVSDSLTDLDFKFSNISEGLSNYSIIDKLVINIVDVLVECKENSS 120
61 MDVLPSCWISBMVQVSDSLTDLDFKFSNISEGLSNYSIIDKLVINIVDVLVECKENSS 120
Db 61 MDVLPSCWISBMVQVSDSLTDLDFKFSNISEGLSNYSIIDKLVINIVDVLVECKENSS 120

QY 121 KDLKSFSPKPEPRLTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 174
121 KDLKSFSPKPEPRLTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 174
Db 121 KDLKSFSPKPEPRLTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180

QY 175 -----KAKNPPGSSSLHMAAMALPALPSLIIGFAGALYWKRR 212
175 -----KAKNPPGSSSLHMAAMALPALPSLIIGFAGALYWKRR 212
Db 181 KPPMLPVAASSLRNDSSSNRKAKNPBGSSSLHMAAMALPALPSLIIGFAGALYWKRR 240

QY 213 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 245
213 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 245
Db 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 5
US-09-224-683-49
Sequence 49, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/557,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989

ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-0448
TELEFAX: 312/474-6300
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-49

Query Match 97.5%; Score 1231; DB 9; Length 273;
Best Local Similarity 89.4%; Pred. No. 8.1e-116;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTOTWILTCIYQLLFNPVLYKTEGICRNRVTNNVQVTKLVANLPKDYMTITLKYPG 60
1 MKKTOTWILTCIYQLLFNPVLYKTEGICRNRVTNNVQVTKLVANLPKDYMTITLKYPG 60
Db 1 MKKTOTWILTCIYQLLFNPVLYKTEGICRNRVTNNVQVTKLVANLPKDYMTITLKYPG 60

QY 61 MDVLPSCWISBMVQVSDSLTDLDFKFSNISEGLSNYSIIDKLVINIVDVLVECKENSS 120
61 MDVLPSCWISBMVQVSDSLTDLDFKFSNISEGLSNYSIIDKLVINIVDVLVECKENSS 120
Db 61 MDVLPSCWISBMVQVSDSLTDLDFKFSNISEGLSNYSIIDKLVINIVDVLVECKENSS 120

QY 121 KDLKSFSPKPEPRLTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 174
121 KDLKSFSPKPEPRLTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 174
Db 121 KDLKSFSPKPEPRLTPEEPFRIFNRSIDAFKDFVVASETSDCVVSTLSPEKDSRVSVT 180

QY 175 -----KAKNPPGSSSLHMAAMALPALPSLIIGFAGALYWKRR 212
175 -----KAKNPPGSSSLHMAAMALPALPSLIIGFAGALYWKRR 212
Db 181 KPPMLPVAASSLRNDSSSNRKAKNPBGSSSLHMAAMALPALPSLIIGFAGALYWKRR 240

QY 213 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 245
213 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 245
Db 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 6
US-09-224-683-61
Sequence 61, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/449,653
 FILING DATE: 24-MAY-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/982,255
 FILING DATE: 25-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/589,701
 FILING DATE: 01-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/573,616
 FILING DATE: 24-AUG-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/537,198
 FILING DATE: 11-JUN-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/422,383
 FILING DATE: 16-OCT-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Clough, David W.
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET NUMBER: 01017/35136
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEFAX: 312/474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 273 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-224-683-61

Query Match 97.5%; Score 1231; DB 9; Length 273;
 Best Local Similarity 89.4%; Pred. No. 8.1e-116;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNVTNNKQVTKLVANLPKQYMTLTKYVG 60
 DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNVTNNKQVTKLVANLPKQYMTLTKYVG 60
 QY 61 MDVLPSCWISSEMVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
 DB 61 MDVLPSCWISSEMVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
 QY 121 KDKKSFSPRLFTPEEFRIENRSDAFKDFVVASETSDCVSSTLSPKGR----- 174
 DB 121 KDKKSFSPRLFTPEEFRIENRSDAFKDFVVASETSDCVSSTLSPKGR----- 180
 QY 175 -----KAKNPDGSSLIHMAAMALPALFSLIIGFAGALYWK 212
 DB 181 KPFMLPVAASLRNDSSSNRKAQNPDDSSLIHMAAMALPALFSLIIGFAGALYWK 240
 QY 213 QPSLTRAVENTIQNEEDNEISMLQEKERFQEV 245
 DB 241 QPSLTRAVENTIQNEEDNEISMLQEKERFQEV 273

RESULT 7
 US-09-005-243-48
 Sequence 48; Application US/09005243
 Patent No. US20020018763A1
 GENERAL INFORMATION:
 APPLICANT: Zsebo, Kristina M.
 APPLICANT: Bosseman, Robert A.
 APPLICANT: Suggs, Sidney V.
 APPLICANT: Martin, Francis H.
 TITLE OF INVENTION: Stem Cell Factor
 NUMBER OF SEQUENCES: 104
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/005,243
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/449,653
 FILING DATE: 24-MAY-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/982,255
 FILING DATE: 25-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/589,701
 FILING DATE: 01-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/573,616
 FILING DATE: 24-AUG-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/537,198
 FILING DATE: 11-JUN-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/422,383
 FILING DATE: 16-OCT-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Clough, David W.
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET NUMBER: 01017/34465
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEFAX: 312/474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 273 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-005-243-48

Query Match 97.1%; Score 1226; DB 9; Length 273;
 Best Local Similarity 89.0%; Pred. No. 2.6e-115;
 Matches 243; Conservative 0; Mismatches 2; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNVTNNKQVTKLVANLPKQYMTLTKYVG 60
 DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNVTNNKQVTKLVANLPKQYMTLTKYVG 60
 QY 61 MDVLPSCWISSEMVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
 DB 61 MDVLPSCWISSEMVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
 QY 121 KDKKSFSPRLFTPEEFRIENRSDAFKDFVVASETSDCVSSTLSPKGR----- 174
 DB 121 KDKKSFSPRLFTPEEFRIENRSDAFKDFVVASETSDCVSSTLSPKGR----- 180
 QY 175 -----KAKNPDGSSLIHMAAMALPALFSLIIGFAGALYWK 212
 DB 181 KPFMLPVAASLRNDSSSNRKAQNPDDSSLIHMAAMALPALFSLIIGFAGALYWK 240
 QY 213 QPSLTRAVENTIQNEEDNEISMLQEKERFQEV 245
 DB 241 QPSLTRAVENTIQNEEDNEISMLQEKERFQEV 273

RESULT 8

US-09-224-683-48
Sequence 48, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Boselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-48

Query Match 97.1%; Score 1226; DB 9; Length 273;

Best Local Similarity 89.0%; Pred. No. 2.6e-115;

Matches 243; Conservative 0; Mismatches 2; Indels 28; Gaps 1;

1 MKKTQWILTCIYQLLFNPLVKTGICRNRTNNVDVTKLVANLPKDYMITLKYYVG 60

Db 1 MKKTQWILTCIYQLLFNPLVKTGICRNRTNNVDVTKLVANLPKDYMITLKYYVG 60

QY 61 MOVLPSCHESEMVQSLDLDKFSNTSEGLSNYSIIDKLVNIYDDLVECKENSS 120

Db 61 MOVLPSCHESEMVQSLDLDKFSNTSEGLSNYSIIDKLVNIYDDLVECKENSS 120

QY 121 KDLKSPKSPPEPRLTPEEPFRIPNRSIDAFKDFVASETSDCVVSTLSPEKG----- 174

Db 121 KDLKSPKSPPEPRLTPEEPFRIPNRSIDAFKDFVASETSDCVVSTLSPEKDSRVST 180

QY 175 -----KANPPQDSSLHMAALPALPSLIIGFAGALYMKR 212

Db 181 KEFMLPVAASLRNDSSSNRKANPPGDSLSLHWPALPALPSLIIGFAGALYMKR 240

QY 213 QPSLTRAVENTIQUEDNEISMLQEKEREPOEV 245

Db 241 QPSLTRAVENTIQUEDNEISMLQEKEREPOEV 273

RESULT 9

US-09-005-243-50
Sequence 50, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Boselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-50

Query Match 96.3%; Score 1215; DB 9; Length 273;
Best Local Similarity 88.3%; Pred. No. 3.3e-114;
Matches 241; Conservative 0; Mismatches 4; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYTNVNVKVTKLVANLPKQVMTTLKYVPG 60
DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYTNVNVKVTKLVANLPKQVMTTLKYVPG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVECVKENS 120
QY 121 KDLKSPKSPERPLFTPEEFRIFNRSIDAFKDFVAVASSETDCVVSSTLSPEKDSRVSVT 174
DB 121 KDLKSPKSPERPLFTPEEFRIFNRSIDAFKDFVAVASSETDCVVSSTLSPEKDSRVSVT 180
QY 175 -----KAKNPBGSSLIHMAAALPALFSLIIGPAGALYMKR 212
DB 181 KPEMLPVAASSLRNDSSSNRKAKNPFGDSSLHMAAALPALFSLIIGPAGALYMKR 240
QY 213 QPSLTRAVENTIOINEEDNEISMLQEKEREFQEV 245
DB 241 QPSLTRAVENTIOINEEDNEISMLQEKEREFQEV 273

RESULT 10
US-09-224-683-50
Sequence 50, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6500
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-50

Query Match 96.3%; Score 1215; DB 9; Length 273;
Best Local Similarity 88.3%; Pred. No. 3.3e-114;
Matches 241; Conservative 0; Mismatches 4; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYTNVNVKVTKLVANLPKQVMTTLKYVPG 60
DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYTNVNVKVTKLVANLPKQVMTTLKYVPG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVECVKENS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDKFSNISSEGLSNYSIIDKLVINIYDDLVECVKENS 120
QY 121 KDLKSPKSPERPLFTPEEFRIFNRSIDAFKDFVAVASSETDCVVSSTLSPEKDSRVSVT 174
DB 121 KDLKSPKSPERPLFTPEEFRIFNRSIDAFKDFVAVASSETDCVVSSTLSPEKDSRVSVT 180
QY 175 -----KAKNPBGSSLIHMAAALPALFSLIIGPAGALYMKR 212
DB 181 KPEMLPVAASSLRNDSSSNRKAKNPFGDSSLHMAAALPALFSLIIGPAGALYMKR 240
QY 213 QPSLTRAVENTIOINEEDNEISMLQEKEREFQEV 245
DB 241 QPSLTRAVENTIOINEEDNEISMLQEKEREFQEV 273

RESULT 11
US-09-005-243-57
Sequence 57, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 266 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-57

Query Match      84.8%; Score 1070.5; DB 9; Length 266;
Best Local Similarity 82.2%; Pred. No. 1.2e-99;
Matches 222; Conservative 10; Mismatches 9; Indels 29; Gaps 6;
```

```
APPLICANT: Zeebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 266 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-57

Query Match      84.8%; Score 1070.5; DB 9; Length 266;
Best Local Similarity 82.2%; Pred. No. 1.2e-99;
Matches 222; Conservative 10; Mismatches 9; Indels 29; Gaps 6;
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QY 121 KOLKSKSPKPEPRLFTPEEFRIENRSDAFKDFVVASSETDCVSSSTLSPEKXAKN-- 178
 118 KQVKS-KSPEPRLFTPEEFRIENRSDAFKDFVVASSETDCVSSSTLSPEKDSVSVT 176
 QY 179 -----PP-----GDSSLHWAMALPALFSLIIGFAGALYWKRRQPS 215
 177 KQFMLPPVVAASLRNDSSSNRKNEDSSIQWAMALPALFSLIIGFAGALYWKRRQPS 236
 Db 216 LTRAVENIQINEEDNEISMLOEKEREFQEV 245
 237 LTRAVENIQINEEDNEISMLOEKEREFQEV 266

RESULT 13
 US-09-005-243-52
 ; Sequence 52, Application US/09005243
 ; Patent No. US20020018763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zsebo, Krisztina M.
 ; APPLICANT: Bosselman, Robert A.
 ; APPLICANT: Suggs, Sidney V.
 ; APPLICANT: Martin, Francis H.
 ; TITLE OF INVENTION: Stem Cell Factor
 ; NUMBER OF SEQUENCES: 104
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/005,243
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/982,255
 ; FILING DATE: 25-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/589,701
 ; FILING DATE: 01-OCT-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/573,616
 ; FILING DATE: 24-AUG-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/537,198
 ; FILING DATE: 11-JUN-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/422,383
 ; FILING DATE: 16-OCT-1989
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clough, David W.
 ; REGISTRATION NUMBER: 36,107
 ; REFERENCE/DOCKET NUMBER: 01017/34465
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/474-6300
 ; TELEFAX: 312/474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 52:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 271 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single

TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-005-243-52

Query Match 80.9%; Score 1020.5; DB 9; Length 271;
 Best Local Similarity 75.6%; Pred. No. 1.4e-94;
 Matches 205; Conservative 18; Mismatches 19; Indels 29; Gaps 3;

QY 3 KQWMLTLCIYQQLLFPNLYVTBEGICNRRVYNNVQDVTKLVAANPKQYMTITLKVPQMD 62
 2 KQWMLTLCIYQQLLFPNLYVTBEGICNRRVYNNVQDVTKLVAANPKQYMTITLKVPQMD 60
 Db 63 VLPSCWISSEWVQSLDLDLDFKSNISBGLSNYSIIDKLVINIVDDLVBCVKNSSKD 122
 61 VLPSCWISSEWVQSLDLDLDFKSNISBGLSNYSIIDKLVINIVDDLVBCVKNSSKD 120
 QY 123 LKSKFSKSPKPEPRLFTPEEFRIENRSDAFKDFVVASSETDCVSSSTLSPEK-- 173
 121 VKSKSKSPKPEPRLFTPEEFRIENRSDAFKDFVVASSETDCVSSSTLSPEKDSVSVTK 180
 Db 174 -----GKXNPPGDSLHWAMALPALFSLIIGFAGALYWKRRQPS 214
 181 PMLPPVVAASLRNDSSSNRKNEDSSIQWAMALPALFSLIIGFAGALYWKRRQPS 240

QY 215 SLTRAVENIQINEEDNEISMLOEKEREFQEV 245
 241 NLRTRAVENIQINEEDNEISMLOEKEREFQEV 271
 Db

RESULT 14
 US-09-224-683-52
 ; Sequence 52, Application US/09224683
 ; Patent No. US20020031491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zsebo, Krisztina M.
 ; APPLICANT: Bosselman, Robert A.
 ; APPLICANT: Suggs, Sidney V.
 ; APPLICANT: Martin, Francis H.
 ; TITLE OF INVENTION: Stem Cell Factor: Composition Claims
 ; NUMBER OF SEQUENCES: 104
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/224,683
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/005,893
 ; FILING DATE: 12-JAN-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/449,653
 ; FILING DATE: 24-MAY-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/982,255
 ; FILING DATE: 25-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/589,701
 ; FILING DATE: 01-OCT-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/573,616
 ; FILING DATE: 24-AUG-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-52

Query Match 80.8%; Score 1020.5; DB 9; Length 271;
Best Local Similarity 75.6%; Pred. No. 1.4e-94;
Matches 205; Conservative 18; Mismatches 19; Indels 29; Gaps 3;

QY 3 KQTWTWLTCTIYQLLLFNPVKTGEGICRRNVTNNVADVTKLVANLPKDYMITLKYPGMD 62
DB 2 KQTWTWLTCTIYQLLLFNPVKTGEGICRRNVTNNVADVTKLVANLPKDYMITLKYPGMD 60
QY 63 VLPSPHCWISBMVQVQLSDSLTDLDDKFSNISEGLSNYSIIDKLVNIYDDIVECVKENSND 122
DB 61 VLPSPHCWISBMVQVQLSDSLTDLDDKFSNISEGLSNYSIIDKLVNIYDDIVECVKENSND 120
QY 123 LKKSFKSPERLFTPEEPFRIFNRSIDAFKDF-VVASETSDCVSSTLSPEK----- 173
DB 121 VKKSKSPERLFTPEEPFRIFNRSIDAFKDFLEVMVSKSECVSSTLSPEKDSRVSVTK 180
QY 174 -----GKKNPQDSSLMHMAALPALFSLIIGFAFGALYKKRP 214
DB 181 PFMVLPVVAASSLNDSSSNRKNTPTEDSSIQAVNALPACFSLVIGFAFGALYKKRP 240
QY 215 SLTRAVENTIQINEEDNEISMLOEKEREFOEV 245
DB 241 NLRTVENVIQINEEDNEISMLOEKEREFOEV 271

RESULT 15
US-09-005-243-51
Sequence 51, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
APPLICANT: Boeselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-51

Query Match 80.4%; Score 1014.5; DB 9; Length 274;
Best Local Similarity 74.8%; Pred. No. 5.8e-94;
Matches 205; Conservative 17; Mismatches 23; Indels 29; Gaps 2;

QY 1 MKQTWTWLTCTIYQLLLFNPVKTGEGICRRNVTNNVADVTKLVANLPKDYMITLKYPG 60
DB 1 MKQTWTWLTCTIYQLLLFNPVKTGEGICRRNVTNNVADVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSPHCWISBMVQVQLSDSLTDLDDKFSNISEGLSNYSIIDKLVNIYDDIVECVKENS 120
DB 61 MDVLPSPHCWISBMVQVQLSDSLTDLDDKFSNISEGLSNYSIIDKLVNIYDDIVECVKENS 120
QY 121 KDKSKSPERLFTPEEPFRIFNRSIDAFKDF-VVASETSDCVSSTLSPEK----- 174
DB 121 ENVKAPKSPERLFTPEEPFRIFNRSIDAFKDFLEVMVSKSECVSSTLSPEKDSRVSVTK 180
QY 175 -----KKNPQDSSLMHMAALPALFSLIIGFAFGALYKK 211
DB 181 TKPMLPVAASSLNDSSSNRKASNSIGSNLQMAAMALPALFSLIIGFAFGALYKK 240
QY 212 RQPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 245
DB 241 KQPNLRTVENVIQINEEDNEISMLOEKEREFOEV 274

Search completed: February 5, 2004, 15:23:27
Job time: 27.3347 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 15:00:43 / Search time 13.8361 Seconds
(without alignments)
1702.889 Million cell updates/sec

Title: US-09-224-683-63

Perfect score: 1262
Sequence: 1 MKKTQWILTCIYQLLFN.....NEEDNEISMLQEKREPOEV 245

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1262	100.0	245	2 B61190	mast cell growth f
2	1231	97.5	273	2 A35974	mast cell growth f
3	1037.5	82.2	274	2 I46574	c-kit ligand - pig
4	1022	81.0	245	2 A37934	mast cell growth f
5	1018.5	80.7	274	2 S47571	stem cell factor,
6	1014.5	80.4	274	2 I46929	stem cell factor -
7	991	78.5	273	2 S65801	stem cell factor f
8	749.5	59.4	202	2 S58313	stem cell growth p
9	721	57.1	201	2 B35974	stem cell factor p
10	605	47.9	253	2 S70367	stem cell factor s
11	584	46.3	287	2 JN0637	stem cell factor p
12	583	46.2	287	2 S70366	stem cell factor p
13	491.5	38.9	124	2 S29052	stem cell factor l
14	175.5	13.9	51	2 B35971	stem cell growth f
15	172.5	13.7	49	2 A35971	mast cell growth f
16	97.5	7.7	402	2 T09062	probable advanced
17	97	7.7	482	2 S37845	transcription init
18	97	7.7	1447	2 F82909	hypothetical prote
19	93.5	7.4	647	2 P90595	conserved ubiquitin
20	93.5	7.4	3227	2 T37964	probable ubiquitin
21	92.5	7.3	512	2 G86773	citrate (pro-3S)-1
22	92.5	7.3	534	2 T23425	hypothetical prote
23	92	7.3	420	2 E90553	hypothetical prote
24	92	7.3	821	2 AD1507	probable secreted
25	92	7.3	1174	1 HJBYDH	helicase (EC 3.6.1
26	91.5	7.3	295	2 AC2939	hypothetical prote
27	91.5	7.3	309	2 D98343	lactose transport
28	91.5	7.3	1993	2 T30902	sodium channel SCA
29	91	7.2	378	2 F64300	formate dehydrogen

30	90.5	7.2	616	2 A69136	ATP-dependent Clp
31	90.5	7.2	774	2 T22309	hypothetical prote
32	90.5	7.2	1675	2 S70770	hypothetical prote
33	90	7.1	411	2 B72012	conserved hypotet
34	90	7.1	411	2 C86613	hypothetical prote
35	89	7.1	1384	2 T26656	hypothetical prote
36	89	7.1	2238	1 RRVUBY	genome polypeptid
37	88.5	7.0	941	2 H84855	phosphoenolpyruv
38	88.5	7.0	1154	2 F71856	hypothetical prote
39	88	7.0	447	2 S74840	replication initia
40	87.5	6.9	246	2 T19850	hypothetical prote
41	87.5	6.9	570	2 S51404	hypothetical prote
42	87.5	6.9	966	2 S26235	phosphoenolpyruv
43	87.5	6.9	1293	2 T27886	hypothetical prote
44	87.5	6.9	1813	2 T19295	hypothetical prote
45	87	6.9	660	2 T22794	hypothetical prote

ALIGNMENTS

RESULT 1.

B61190
mast cell growth factor, short form precursor - human
N/Alternate names: kit ligand, short form; stem cell factor, short form
C/Species: Homo sapiens (man)
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
C/Accession: B61190
R/Anderson, D.M.; Williams, D.E.; Tushinski, R.; Gimpe, S.; Eisenman, J.; Cannizzaro, L.
Cell Growth Differ. 2, 373-378, 1991
A/Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localiza
A/Reference number: A61190; MUID:92172791; PMID:1724381
A/Accession: B61190
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Comment: Alternative splicing produces this short form in which a predicted cleavage s
A/Comment: Alternative splicing produces this short form in which a predicted cleavage s
C/Genes: GDB:MGF
A/Cross-References: GDB:128026; OMIM:184745
A/Map position: 12q22-12q22
C/Superfamily: mouse mast cell growth factor
C/Keywords: alternative splicing; glycoprotein; transmembrane protein
F/1-25/Domain: signal sequence #status predicted <SIG>
F/187-209/Domain: transmembrane #status predicted <TMN>
F/190-97,118,145/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match

Best Local Similarity 100.0%; Score 1262; DB 2; Length 245;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVQVTVLVANLPEDYMITLKYPVG	60
DB	1	MKKTQWILTCIYQLLFNPLVKTGICRNRVTNNVQVTVLVANLPEDYMITLKYPVG	60
QY	61	MDVLPSCWISPMVQLSDSLTDLDDKFSNISEGASNTSIIDKLVNIYDDLVCEYKENS	120
DB	61	MDVLPSCWISPMVQLSDSLTDLDDKFSNISEGASNTSIIDKLVNIYDDLVCEYKENS	120
QY	121	KOLKSFSPSPRLTPEEPFRIFNRSIDAFQVVASSETSCVASTLSPKGAQKPP	180
DB	121	KOLKSFSPSPRLTPEEPFRIFNRSIDAFQVVASSETSCVASTLSPKGAQKPP	180
QY	181	GDSLSHMAAMALPALFSIIGFAGALYMKRQPSLTRAVENTIQNEEDNEISMLQEKER	240
DB	181	GDSLSHMAAMALPALFSIIGFAGALYMKRQPSLTRAVENTIQNEEDNEISMLQEKER	240
QY	241	EFQEV 245	
DB	241	EFQEV 245	

RESULT 2

A35974
mast cell growth factor precursor - human
N:Alternate names: kit ligand; stem cell factor
C:Species: Homo sapiens (man)
C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C:Accession: A35974; A61190
R:Martin, F.H.; Sugars, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.F.
S, J.C.; Patel, A.C.; Fisher, E.F.; Erjavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev, R.
Cell 63, 203-211, 1990
A>Title: Primary structure and functional expression of rat and human stem cell factor D
A:Reference number: A35974; MUID:91004219; PMID:2208279
A:Accession: A35974
A:Molecule type: mRNA
A:Residues: 1-273 <MAR>
A:Cross-references: GB:M59664; NID:9337933; PIDN:AAA5670.1; PID:9337934
R:Anderson, D.M.; Williams, D.E.; Tushinski, R.; Gimpel, S.; Eisenman, J.; Cammizzaro, L.
Cell Growth Differ. 2, 373-378, 1991
A>Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localiza
A:Reference number: A61190; MUID:92172791; PMID:1724381
A:Accession: A61190
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-273 <AND>
A:Gene: GDB:MGF
A:Cross-references: GDB:128026; OMIM:184745
A:Map position: 12q22-12q22
C:Superfamily: mouse mast cell growth factor
C:Keywords: alternative splicing; extracellular protein; glycoprotein; transmembrane pro
F.1-25/Domain: signal sequence #status predicted <Sig>
F.26-273/Product: mast cell growth factor #status predicted <MCS>
F.26-189/Product: (or 26-190) mast cell growth factor; soluble form #status predicted <M
F.90,97,118,145,195/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 97.5%; Score 1231; DB 2; Length 273;
Best Local Similarity 89.4%; Pred. No. 1.9e-92;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;
QY 1 MKKTQWITTCIYQLLNFPLVKTGICRRRVNNVQVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWITTCIYQLLNFPLVKTGICRRRVNNVQVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSLDLDLDRKSNISEGLSNYSIIDKLVINIVDDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQSLDLDLDRKSNISEGLSNYSIIDKLVINIVDDLVCEKENS 120
QY 121 KDLKSFSPKPEPRLFTPEEFRIENRSIDAFKDFVASETSDCVSSTLSPEKGV----- 174
DB 121 KDLKSFSPKPEPRLFTPEEFRIENRSIDAFKDFVASETSDCVSSTLSPEKGVSVT 180
QY 175 -----KAKNPPGSSLSHMAAMLPALFSLITGPAFGALYMKK 212
DB 181 KPEFMPPLVPAASSLRNDSSSNRKAQNPDPDSSLSHMAAMLPALFSLITGPAFGALYMKK 240
QY 213 OPSLTRAVENTIOINEEDNEISMLQEKERFQEV 245
DB 241 OPSLTRAVENTIOINEEDNEISMLQEKERFQEV 273

RESULT 3
146575
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jul-2000
C:Accession: 146575
R:Zhang, Z.; Anthony, R.V.
Biol. Reprod. 50, 95-102, 1994
A>Title: Porcine stem cell factor/C-kit ligand; its molecular cloning and localization w
A:Reference number: 146575; MUID:94146218; PMID:7508758
A:Accession: 146575
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-274 <ZHA>
A:Cross-references: GB:L07786; NID:9164420; PIDN:AAA5670.1; PID:9164421
C:Superfamily: mouse mast cell growth factor
Query Match 82.2%; Score 1037.5; DB 2; Length 274;
Best Local Similarity 75.2%; Pred. No. 9.6e-77;
Matches 206; Conservative 22; Mismatches 17; Indels 29; Gaps 2;
QY 1 MKKTQWITTCIYQLLNFPLVKTGICRRRVNNVQVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWITTCIYQLLNFPLVKTGICRRRVNNVQVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSLDLDLDRKSNISEGLSNYSIIDKLVINIVDDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQSLDLDLDRKSNISEGLSNYSIIDKLVINIVDDLVCEKENS 120
QY 121 KDLKSFSPKPEPRLFTPEEFRIENRSIDAFKDFVASETSDCVSSTLSPEKGV----- 174
DB 121 ENVKSSKSPKPEPRLFTPEEFRIENRSIDAFKDFVASETSDCVSSTLSPEKGVSV 180
QY 175 -----KAKNPPGSSLSHMAAMLPALFSLITGPAFGALYMKK 211
DB 181 TKPFMLPVAASSLRNDSSSNRKAQNPDPDSSLSHMAAMLPALFSLITGPAFGALYMKK 240
QY 212 RQPSLTRAVENTIOINEEDNEISMLQEKERFQEV 245
DB 241 KQPNLTRAVENIOINEEDNEISMLQEKERFQEV 274

RESULT 4
A37934
mast cell growth factor precursor (version 2) - mouse
N:Alternate names: KL-2 protein
C:Species: Mus musculus (house mouse)
C>Date: 26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change 21-Jul-2000
C:Accession: A37934; B43751
R:Flanagan, J.G.; Chan, D.C.; Leder, P.
Cell 64, 1025-1035, 1991
A>Title: Transmembrane form of the kit ligand growth factor is determined by alternative
A:Reference number: A37934; MUID:91160046; PMID:1705866
A:Accession: A37934
A:Molecule type: mRNA
A:Residues: 1-245 <FLA>
A:Cross-references: GB:M64262
R:Huang, E.J.; Nocka, K.H.; Buck, J.; Besmer, P.
Mol. Biol. Cell 3, 349-362, 1992
A>Title: Differential expression and processing of two cell associated forms of the kit-
A:Reference number: A43751; MUID:92330001; PMID:1378327
A:Accession: B43751
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-173,'R',175-186,'L',188-245 <HDA>
A:Cross-references: GB:S04534
A>Note: the authors translated the codon TTG for residue 187 as Trp
C:Superfamily: mouse mast cell growth factor
Query Match 81.0%; Score 1022; DB 2; Length 245;
Best Local Similarity 80.8%; Pred. No. 1.5e-75;
Matches 198; Conservative 19; Mismatches 28; Indels 0; Gaps 0;
QY 1 MKKTQWITTCIYQLLNFPLVKTGICRRRVNNVQVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWITTCIYQLLNFPLVKTGICGNPVTDNDVDTIKLVANLPKDYMITLANYAG 60
QY 61 MDVLPSCWISSEWVQSLDLDLDRKSNISEGLSNYSIIDKLVINIVDDLVCEKENS 120
DB 61 MDVLPSCWISSEWVQSLDLDLDRKSNISEGLSNYSIIDKLVINIVDDLVCEKENS 120
QY 121 KDLKSFSPKPEPRLFTPEEFRIENRSIDAFKDFVASETSDCVSSTLSPEKGVAKK 180
DB 121 KDLKSFSPKPEPRLFTPEEFRIENRSIDAFKDFVASETSDCVSSTLSPEKGVAKK 180
QY 181 GDSLSHMAAMLPALFSLITGPAFGALYMKK 240

Db 181 EDGGLMTAMALPALISLVIGAFAGALYWKQSLTRAVENTQINEEDNEISMLQOKR 240
 Oy 241 EFOEV 245
 Db 241 EFOEV 245

RESULT 5

stem cell factor, longer isoform - bovine
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
 C/Accession: S47571
 R/Zhou, J.H.; Hikono, H.; Ohtaki, M.; Kubota, T.; Sakurai, M.
 Biochim. Biophys. Acta 1223, 148-150, 1994
 A/Title: Cloning and characterization of cDNAs encoding two normal isoforms of bovine st
 A/Reference number: S47571; MUID:94339176; PMID:7520283
 A/Accession: S47571
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-274 <ZHO>
 A/Cross-references: EMBL:D88934; NID:g538520; PIDN:BA06061.1; PID:g538521
 C/Superfamily: mouse mast cell growth factor

Query Match 80.7%; Score 1018.5; DB 2; Length 274;
 Best Local Similarity 74.1%; Pred. No. 3.3e-75;
 Matches 203; Conservative 20; Mismatches 22; Indels 29; Gaps 2;

Oy 1 MKKTQWILTCIYLQLLFNPVLTGICGNRVTVNNKDYTKLVANLPKDYMITLKYPG 60
 Db 1 MKKTQWILTCIYLQLLFNPVLTGICGNRVTVNNKDYTKLVANLPKDYMITLKYPG 60
 Oy 61 MDVLPSCWISSEWVQSLDSDLTLDKFSNISEGLSNYSIIIDKLVNIYDVLVECVKENS 120
 Db 61 MDVLPSCWISSEWVQSLDSDLTLDKFSNISEGLSNYSIIIDKLVNIYDVLVECVKENS 120
 Oy 121 KDLKKSFKSPERLFTPEEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPKGF----- 174
 Db 121 ENVKKSKSPERQFTPEKFFGIFNKSIDAFKDFVAVASGMSGCVSSTSPKDSRVSV 180
 Oy 175 -----KAKNPPGDSLSHMAAMALPALFSIIIGFAGALYWK 211
 Db 181 TKPFMLPVVAASLRNDSSSNRKASNSIDSSIQMAVALPAFFSLVIGAFAGAFYWK 240
 Oy 212 ROPSITRAVENTQINEEDNEISMLQOKERFQEV 245
 Db 241 KQPNLTRVTENQINEEDNEISMLQOKERFQEV 274

RESULT 6

146929
 stem cell factor - dog
 C/Species: Canis lupus familiaris (dog)
 C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 21-Jul-2000
 C/Accession: I46929
 R/Shull, R.M.; Suggs, S.V.; Langley, K.E.; Okino, K.H.; Jacobsen, F.W.; Martin, F.H.
 Exp. Hematol. 20, 1118-1124, 1992
 A/Title: Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic p
 A/Reference number: I46929; MUID:93106145; PMID:1281786
 A/Accession: I46929
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-274 <SHU>
 A/Cross-references: GB:S53329; NID:g262240; PIDN:AA24619.1; PID:g262241
 C/Superfamily: mouse mast cell growth factor

Query Match 80.4%; Score 1014.5; DB 2; Length 274;
 Best Local Similarity 74.8%; Pred. No. 7e-75;
 Matches 203; Conservative 17; Mismatches 23; Indels 29; Gaps 2;

Oy 1 MKKTQWILTCIYLQLLFNPVLTGICGNRVTVNNKDYTKLVANLPKDYMITLKYPG 60
 Db 1 MKKTQWILTCIYLQLLFNPVLTGICGNRVTVNNKDYTKLVANLPKDYMITLKYPG 60

Db 1 MKKTQWILTCIYLQLLFNPVLTGICGNRVTVNNKDYTKLVANLPKDYMITLKYPG 60
 Oy 61 MDVLPSCWISSEWVQSLDSDLTLDKFSNISEGLSNYSIIIDKLVNIYDVLVECVKENS 120
 Db 61 MDVLPSCWISSEWVQSLDSDLTLDKFSNISEGLSNYSIIIDKLVNIYDVLVECVKENS 120
 Oy 121 KDLKKSFKSPERLFTPEEFRIFNRSIDAFKDF-VVASETSDCVVSTLSPKGF----- 174
 Db 121 ENVKKSKSPERLFTPEEFRIFNRSIDAFKDFVAVASGMSGCVSSTSPKDSRVSV 180
 Oy 175 -----KAKNPPGDSLSHMAAMALPALFSIIIGFAGALYWK 211
 Db 181 TKPFMLPVVAASLRNDSSSNRKASNSIDSSIQMAVALPAFFSLVIGAFAGALYWK 240
 Oy 212 ROPSITRAVENTQINEEDNEISMLQOKERFQEV 245
 Db 241 KQPNLTRVTENQINEEDNEISMLQOKERFQEV 274

RESULT 7

stem cell growth factor - mouse
 N/Alternate names: hematopoietic growth factor KL; ligand steel factor; stem cell facto
 C/Species: Mus musculus (house mouse)
 C/Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 01-Dec-2000
 C/Accession: S65801; A43751; A35976; A35972; A35973; I48768
 R/Bedell, M.A.; Copeland, N.G.; Jenkins, N.A.
 Genetics 142, 927-934, 1996
 A/Title: Multiple pathways for Steel regulation suggested by genomic and sequence analy
 A/Reference number: S65801; MUID:97002551; PMID:884989
 A/Accession: S65801
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-273 <BED>

A/Cross-references: EMBL:U44725; NID:g1172215; PIDN:AAC2447.1; PID:g1172216
 R/Huang, E.J.; Nocka, K.H.; Buck, J.; Besmer, P.
 Mol. Biol. Cell 3, 349-362, 1992
 A/Title: Differential expression and processing of two cell associated forms of the kit
 A/Reference number: A43751; MUID:92330001; PMID:1378927

A/Accession: A43751
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-214, 'V', 216-273 <HUA>
 A/Cross-references: GB:S40364; NID:g251668; PIDN:AA22554.2; PID:g5705957
 A/Note: The authors translated the codon TTG for residue 215 as TTP
 R/Huang, E.; Nocka, K.; Beier, D.R.; Chu, T.Y.; Buck, J.; Lahm, H.W.; Wellner, D.; Leder
 Cell 63, 225-233, 1990
 A/Title: The hematopoietic growth factor KL is encoded by the sl locus and is the ligand
 A/Reference number: A35976; MUID:91004221; PMID:1698557
 A/Accession: A35976
 A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA
 A/Residues: 1-206, 'S', 208-270 <HU2>
 A/Cross-references: GB:M38511
 R/Anderson, D.M.; Lyman, S.D.; Baird, A.; Wignall, J.M.; Eisenman, J.; Rauch, C.; March
 Cell 63, 235-243, 1990
 A/Title: Molecular cloning of mast cell growth factor, a hematopoietin that is active in
 A/Reference number: A35977; MUID:91004223; PMID:1698558
 A/Accession: A35977
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-273 <AND>
 A/Cross-references: GB:M57647; GB:M38436; NID:g199151; PIDN:AAA39538.1; PID:g199152
 R/Copeland, N.G.; Gilbert, D.J.; Cho, B.C.; Donovan, P.O.; Jenkins, N.A.; Cosman, D.; An
 Cell 63, 175-183, 1990
 A/Title: Mast cell growth factor maps near the steel locus on mouse chromosome 10 and is
 A/Reference number: A35972; MUID:91004216; PMID:1698554
 A/Accession: A35972
 A/Status: preliminary

A/Molecule type: mRNA
 A/Residues: 26-53 <COP>
 A/Cross-references: GB:M59912
 R/Sebo, K.M.; Williams, D.A.; Geisler, E.N.; Brody, V.C.; Martin, F.H.; Atkins, H.L.;

; Catnach, B.M.; Galli, S.J.; Sugas, S.V.
 Cell 63, 213-224, 1990
 A:Title: Stem cell factor is encoded at the Sl locus of the mouse and is the ligand for
 A:Reference number: A35975; MUID:91004220; PMID:1698556
 A:Accession: A35975
 A:Molecule type: mRNA
 A:Residues: 1-201 <5SE>
 A:Cross-references: GB:M59915; NID:9200935; PIDN:AAA40095.1; PID:9554271
 R:Sebo, K.M.; Wypych, J.; McNeice, I.K.; Lu, H.S.; Smith, K.A.; Karkare, S.B.; Sachdev,
 A:Langley, K.E.
 Cell 63, 195-201, 1990
 A:Title: Identification, purification, and biological characterization of hematopoietic
 A:Reference number: A35973; MUID:91004218; PMID:2208278
 A:Accession: A35973
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 21-29, 'R', 'J', '39' <2S2>
 R:Brannan, C.I.; Bedell, M.A.; Resnick, J.L.; Eppig, J.J.; Handel, M.A.; Williams, D.E.;
 Genes Dev. 6, 1832-1842, 1992
 A:Title: Developmental abnormalities in Steel17H mice result from a splicing defect in
 A:Reference number: A44071; MUID:93012940; PMID:1383087
 A:Accession: I48768
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-206, 'S', '208-273' <RES>
 A:Cross-references: EMBL:X68989; NID:9395283; PIDN:CAA48778.1; PID:9395284
 C:Genetics:
 A:Gene: SLF
 A:Map position: 10
 A:Superfamily: mouse mast cell growth factor
 C:Keywords: extracellular protein; glycoprotein; transmembrane protein

Query Match 78.5%; Score 991; DB 2; Length 273;

Best Local Similarity 72.2%; Pred. No. 5.6e-75;
 Matches 197; Conservative 19; Mismatches 29; Indels 28; Gaps 1;

QY 1 MKKTQWIIITCIYQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYPVG 60
 DB 1 MKKTQWIIITCIYQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYPVG 60
 QY 61 MDVLPSCWISSEWVQSLDLDLDFKSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCWISSEWVQSLDLDLDFKSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KULKSKFSPERPLTPPEPRFRINRSIDAKDFVVAASSETSDCVVSTLSPEK----- 174
 DB 121 KULKSKFSPERPLTPPEPRFRINRSIDAKDFVVAASSETSDCVVSTLSPEK----- 174
 QY 121 KNIKESPKRPERFSPPEPRFISIDAFKDFVVAASSETSDCVVSTLSPEKDSRVSVT 180
 DB 121 KNIKESPKRPERFSPPEPRFISIDAFKDFVVAASSETSDCVVSTLSPEKDSRVSVT 180
 QY 175 -----KAKNPQDPSLHMAALPALFSLIIGFAFGALYWKRR 212
 DB 181 KPEMLPVAASSLRNDSNNRKAAPEDSGIQWTRMALPALISLVIGFAGALYWKRR 240
 QY 213 QPSLTRAVENIQINEEDNEISMLQEKEREFOEV 245
 DB 241 QSSLTRAVENIQINEEDNEISMLQEKEREFOEV 273

RESULT 8

S58313
 stem cell factor precursor - sheep (fragment)
 C:Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)
 C:Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000
 C:Accession: S58313
 R:McInnes, C.J.; Logan, M.; Falconer, V.M.; Rawlins, P.; Huntly, J.; Haig, D.
 submitted to the EMBL Data Library, August 1995
 A:Description: Molecular cloning and biological activity of ovine stem cell factor.
 A:Reference number: S58313
 A:Accession: S58313
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-202 <MC1>
 A:Cross-references: EMBL:Z50743; NID:9940807; PIDN:CAA90620.1; PID:9940808
 C:Superfamily: mouse mast cell growth factor

Query Match 59.4%; Score 749.5; DB 2; Length 202;
 Best Local Similarity 83.9%; Pred. No. 1.5e-53;
 Matches 146; Conservative 15; Mismatches 12; Indels 1; Gaps 1;

QY 1 MKKTQWIIITCIYQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYPVG 60
 DB 1 MKKTQWIIITCIYQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYPVG 60
 QY 61 MDVLPSCWISSEWVQSLDLDLDFKSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCWISSEWVQSLDLDLDFKSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KULKSKFSPERPLTPPEPRFRINRSIDAKDFVVAASSETSDCVVSTLSPEK 173
 DB 121 KULKSKFSPERPLTPPEPRFRINRSIDAKDFVVAASSETSDCVVSTLSPEK 173
 QY 121 KNIKESPKRPERFSPPEPRFISIDAFKDFVVAASSETSDCVVSTLSPEK 174
 DB 121 KNIKESPKRPERFSPPEPRFISIDAFKDFVVAASSETSDCVVSTLSPEK 174

RESULT 9

B35974
 stem cell factor protein precursor - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
 C:Accession: B35974; A39805
 R:Martin, F.H.; Sugas, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.F.
 s; J.C.; Patel, A.C.; Fisher, E.F.; Erjavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev, R
 Cell 63, 203-211, 1990
 A:Title: Primary structure and functional expression of rat and human stem cell factor D
 A:Reference number: A35974; MUID:91004219; PMID:2208279
 A:Accession: B35974
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-201 <MAR>
 A:Cross-references: GB:M59966; NID:9206861; PIDN:AAA42117.1; PID:9554507
 R:Lu, H.S.; Clogston, C.L.; Wypych, J.; Fausset, P.R.; Lauren, S.; Mendiaz, E.A.; Zsebo,
 J. Biol. Chem. 266, 8102-8107, 1991
 A:Title: Amino acid sequence and post-translational modification of stem cell factor iso
 A:Reference number: A39805; MUID:91217037; PMID:1708771
 A:Accession: A39805
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 'E', '27-190' <LUA>
 C:Superfamily: mouse mast cell growth factor

Query Match 57.1%; Score 721; DB 2; Length 201;

Best Local Similarity 79.8%; Pred. No. 3e-51;
 Matches 138; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKKTQWIIITCIYQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYPVG 60
 DB 1 MKKTQWIIITCIYQLLFNPLVKTGICRNRVTNNVQVTKLVANLPKDYMITLKYPVG 60
 QY 61 MDVLPSCWISSEWVQSLDLDLDFKSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCWISSEWVQSLDLDLDFKSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KULKSKFSPERPLTPPEPRFRINRSIDAKDFVVAASSETSDCVVSTLSPEK 173
 DB 121 KULKSKFSPERPLTPPEPRFRINRSIDAKDFVVAASSETSDCVVSTLSPEK 173
 QY 121 KNIKESPKRPERFSPPEPRFISIDAFKDFVVAASSETSDCVVSTLSPEK 173
 DB 121 KNIKESPKRPERFSPPEPRFISIDAFKDFVVAASSETSDCVVSTLSPEK 173

RESULT 10

S70367
 stem cell factor short form precursor - quail
 C:Species: Coturnix coturnix (quail)
 C:Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
 C:Accession: S70367
 R:Petitje, J.N.; Kulik, M.J.
 Biochim. Biophys. Acta 1307, 149-151, 1996
 A:Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell fac
 A:Reference number: S70366; MUID:96283808; PMID:8679698
 A:Accession: S70367
 A:Molecule type: mRNA

A:Residues: 1-253 <PET>
 A:Cross-references: EMBL:U43079; NID:g1150877; PIDN:AAC59934.1; PID:g1150878
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: growth factor; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-253/Product: stem cell factor short form #status predicted <MAT>
 F:192-216/Domain: transmembrane #status predicted <TM>

Query Match 47.9%; Score 605; DB 2; Length 253;
 Best Local Similarity 49.8%; Pred. No. 1e-41; Indels 8; Gaps 5;
 Matches 126; Conservative 48; Mismatches 71; Indels 8; Gaps 5;

QY 1 MKKTQWITTCIYQLLEFNPVKTGICRNVYNNVKYLVANLPKDYMITLKVYV 60
 1 MKKAQWITTCFCQLQLLNPVKTQSSCGNPYTDVNDIAKLVGNLPNDYITLKVYV 60
 DB 61 MDVLPSCWISSENVQVLSLTLDFK---SNISGLSNYSITDKLVNIVDLVCEVKE 117
 61 MDSLPHNCWHLMWVPEFSRSLHNLQKFVDISDMSDVLSNYSITINNLTIRINDLMACLA 120
 QY 118 NSSKD-LKKSFKSPPEPRLFTPEEPFRIPNRSIDAFDPVVASSTDCVVSSTL-SPEK 175
 121 DKKKDFIKENGLHYEDRFPENFRILNRTILEVKEFADSLDKNDICIMPSTVETPE 180
 DB 176 AKNPFGDSSLHMAAMALPALFSLIIGFAGALYMKKROP-SLTRAVENTIQIN--EEDNEI 232
 181 ALGFSSSSLOGISIALTSLSLIGILGVIYMKKTHPKSRPESNETTQCHGQENEL 240
 QY 233 SMLQEKREPEQEV 245
 241 SMLQEKREHLQV 253

RESULT 11

JN0637
 stem cell factor precursor - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 21-Jul-2000
 C/Accession: JN0637
 R:Zhou, J.H.; Ohkaki, M.; Sakurai, M.
 Gene 127, 269-270, 1993
 A>Title: Sequence of a cDNA encoding chicken stem cell factor.
 A:Reference number: JN0637; MID:93273244; PMID:7684722
 A:Accession: JN0637
 A:Molecule type: mRNA
 A:Residues: 1-287 <ZHO>
 A:Cross-references: GB:D13516; NID:g9391648; PIDN:BA02733.1; PID:g9391649
 A:Experimental source: brain
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: growth factor; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-287/Product: stem cell factor #status predicted <MAT>
 F:226-248/Domain: transmembrane #status predicted <TM>

Query Match 46.3%; Score 584; DB 2; Length 287;
 Best Local Similarity 44.6%; Pred. No. 6.2e-40; Indels 42; Gaps 7;
 Matches 128; Conservative 46; Mismatches 71; Indels 42; Gaps 7;

QY 1 MKKTQWITTCIYQLLEFNPVKTGICRNVYNNVKYLVANLPKDYMITLKVYV 60
 1 MKKAQWITTCFCQLQLLNPVKAQSSCGNPYTDVNDIAKLVGNLPNDYITLKVYV 60
 DB 61 MDVLPSCWISSENVQVLSLTLDFKSNISGLSNYSITDKLVNIVDLVCEVKE 117
 61 MDSLPHNCWHLMWVPEFSRSLHNLQKFSDISDMSDVLSNYSITINNLTIRINDLMACLA 120
 QY 118 NSSKD-LKKSFKSPPEPRLFTPEEPFRIPNRSIDAFDPVVASSTDCVVSSTL-SPEK 175
 121 DKKKDFIKENGLHYEDRFPENFRILNRTILEVKEFADSLDKNDICIMPSTVETPE 180
 DB 176 AKNPFGDSSLHMAAMALPALFSLIIGFAGALYMKKROP-SLTRAVENTIQIN--EEDNEI 232
 181 ALGFSSSSLOGISIALTSLSLIGILGVIYMKKTHPKSRPESNETTQCHGQENEL 240

QY 202 FAFGALYMKKROP-SLTRAVENTIQIN--EEDNEISMLQEKREPEQEV 245
 241 FILGAIYMKKTHPKSRPESNETTQCHGQENEISMLQEKREHLQV 287

RESULT 12

stem cell factor long form precursor - quail
 S70366
 C:Species: Coturnix coturnix (quail)
 C>Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
 C/Accession: S70366
 R:Petitje, J.N.; Kulik, M.J.
 Biochim. Biophys. Acta 1307, 149-151, 1996
 A>Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell fac
 A:Reference number: S70366; MID:96283808; PMID:8679698
 A:Accession: S70366
 A:Molecule type: mRNA
 A:Residues: 1-287 <PET>
 A:Cross-references: EMBL:U43078; NID:g1150875; PIDN:AAC59933.1; PID:g1150876
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: growth factor; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-287/Product: stem cell factor long form #status predicted <MAT>
 F:226-250/Domain: transmembrane #status predicted <TM>

Query Match 46.2%; Score 583; DB 2; Length 287;
 Best Local Similarity 44.3%; Pred. No. 7.4e-40; Indels 42; Gaps 7;
 Matches 127; Conservative 47; Mismatches 71; Indels 42; Gaps 7;

QY 1 MKKTQWITTCIYQLLEFNPVKTGICRNVYNNVKYLVANLPKDYMITLKVYV 60
 1 MKKAQWITTCFCQLQLLNPVKTQSSCGNPYTDVNDIAKLVGNLPNDYITLKVYV 60
 DB 61 MDVLPSCWISSENVQVLSLTLDFK---SNISGLSNYSITDKLVNIVDLVCEVKE 117
 61 MDSLPHNCWHLMWVPEFSRSLHNLQKFVDISDMSDVLSNYSITINNLTIRINDLMACLA 120
 QY 118 NSSKD-LKKSFKSPPEPRLFTPEEPFRIPNRSIDAFDPVVASSTDCVVSSTL-SPEK 175
 121 DKKKDFIKENGLHYEDRFPENFRILNRTILEVKEFADSLDKNDICIMPSTVETPE 180
 DB 176 AKNPFGDSSLHMAAMALPALFSLIIGFAGALYMKKROP-SLTRAVENTIQIN--EEDNEI 232
 181 ALGFSSSSLOGISIALTSLSLIGILGVIYMKKTHPKSRPESNETTQCHGQENEL 240
 QY 202 FAFGALYMKKROP-SLTRAVENTIQIN--EEDNEISMLQEKREPEQEV 245
 241 FILGAIYMKKTHPKSRPESNETTQCHGQENEISMLQEKREHLQV 287

RESULT 13

S29052
 stem cell factor - human (fragments)
 C:Species: Homo sapiens (man)
 C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 C/Accession: S29052
 R:Lu, H.S.; Clogston, C.L.; Wypych, J.; Parker, V.P.; Lee, T.D.; Swiderak, K.; Baltera J
 Arch. Biochem. Biophys. 298, 150-158, 1992
 A>Title: Post-translational processing of membrane-associated recombinant human stem cell
 A:Reference number: S29052; MID:92398336; PMID:1381905
 A:Accession: S29052
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13;14-30;31-46;47-59;60-86;87-95;96-107;108-124 <LUH>
 C:Superfamily: mouse mast cell growth factor

Query Match 38.9%; Score 491.5; DB 2; Length 124;
 Best Local Similarity 72.3%; Pred. No. 6.6e-33; Indels 41; Gaps 4;
 Matches 107; Conservative 0; Mismatches 0; Indels 41; Gaps 4;

QY 26 EIGCNRYVNNVKDYTKLVANLPKDYMITLKVPGMDVLPSCWISSENVQVLSLTL 85

```
Db      1 EGIICRNRYTNVNVK-----DVLPSHCWISSEWVQLS----- 30
QY      86 DKFSNTSEGLSNYSIIDKLVNIIVDLVECKENSSKDLKSKFSPPEPRLFTPEEPFRIN 145
Db      31 DKFSNTSEGLSNYSITI-----DDLVECKENSSKDLKSKFSPPEPRLFTPEEPFRIN 83
QY      146 RSIDAFKDFVVASETSDCVVSSVTLSPK 173
Db      84 RSI----DFVVASETSDCVVSSVTLSPK 107
```

```
RESULT 14
B35971
mast cell growth factor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C:Accession: B35971
R:Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I
Cell 63, 167-174, 1990
A:Title: Identification of a ligand for the c-kit proto-oncogene.
A:Reference number: A35971; MUID:91004215; PMID:1698553
A:Accession: B35971
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-51 <WIL>
C:Superfamily: mouse mast cell growth factor
C:Keywords: transmembrane protein
```

```
Query Match      13.9%; Score 175.5; DB 2; Length 51;
Best Local Similarity 72.3%; Pred. No. 9e-08;
Matches 34; Conservative 5; Mismatches 7; Indels 1; Gaps 1;
```

```
QY      28 ICRNRYTNVNVKDTKLIVANLPKDYMITLKYPGMDVLPSCWISEMV 74
Db      3 ICGNPVTDVVKDITKLIVANLPNDYMITLVNAGMDVLPSP-WMLDDMI 48
```

```
RESULT 15
A35971
mast cell growth factor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C:Accession: A35971
R:Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I
Cell 63, 167-174, 1990
A:Title: Identification of a ligand for the c-kit proto-oncogene.
A:Reference number: A35971; MUID:91004215; PMID:1698553
A:Accession: A35971
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-49 <WIL>
C:Superfamily: mouse mast cell growth factor
C:Keywords: transmembrane protein
```

```
Query Match      13.7%; Score 172.5; DB 2; Length 49;
Best Local Similarity 73.5%; Pred. No. 1.5e-07;
Matches 36; Conservative 4; Mismatches 6; Indels 3; Gaps 2;
```

```
QY      28 ICRNRYTNVNVKDTKLIVANLPKDYMITLKYPGMDVLPSCWISEMV 76
Db      3 ICGNPVTDVVKDITKLIVANLPNDYMITLVNAGMDVLPSP-WY-DWVIQ 48
```

Search completed: February 5, 2004, 15:08:22
Job time : 14.8361 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 14:42:38 ; Search time 7.76171 Seconds
(without alignments)
1484.408 Million cell updates/sec

Title: US-09-224-683-63

Perfect score: 1262

Sequence: 1 MKKTQWILTCIYLQLLFN.....NEEDNEISWLGKEREFEQEV 245

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1231	97.5	273	1 SCF_HUMAN	P21583 homo sapien
2	1053.5	83.5	274	1 SCF_HORSE	Q95md2 equus caball
3	1051.5	83.3	274	1 SCF_FELCA	P79169 felis silve
4	1037.5	82.2	274	1 SCF_PIG	Q29030 sus scrofa
5	1021.5	80.9	274	1 SCF_CARIH	Q95m19 capra hircu
6	1018.5	80.7	274	1 SCF_BOVIN	Q28132 bos taurus
7	1014.5	80.4	274	1 SCF_CANFA	Q06220 canis famli
8	1014.5	80.4	274	1 SCF_MUSVI	Q95n18 musccla vis
9	992	78.6	273	1 SCF_RAT	P21581 rattus norv
10	991	78.5	273	1 SCF_MOUSE	P20826 mus musculu
11	990.5	78.5	267	1 SCF_SHEEP	P79368 ovis aries
12	584	46.3	287	1 SCF_CHICK	Q09108 gallus gall
13	583	46.2	287	1 SCF_COTJA	Q09314 coturnix co
14	99	7.8	496	1 MURE_WIGBR	Q8d221 wigglewort
15	97	7.7	482	1 T2EA_YEAST	P36100 saccharomyc
16	94.5	7.5	403	1 RAGE_MOUSE	Q62151 mus musculu
17	91	7.2	378	1 FDHA_METJA	Q60314 methanococc
18	91	7.2	402	1 RAGE_RAT	Q63495 rattus norv
19	91	7.2	981	1 SC44_RICFE	Q9a377 rickettsia
20	90.5	7.2	1675	1 POL_RTBVP	P27502 rice tungro
21	90	7.1	267	1 PKI_NPVHZ	P41719 heliothis z
22	90	7.1	411	1 RMUC_CHIRN	Q92687 chlamydia p
23	90	7.1	1039	1 PDP2_ARATH	Q9m968 arabidopsis
24	89	7.1	2238	1 RRPL_BUNYW	P20470 bunyameera
25	88	7.0	447	1 DNAA_SYNY3	P49955 synchocyst
26	87.5	6.9	966	1 SCF_MEDSA	Q02715 medicago sa
27	87.5	6.9	1175	1 SRS2_YEAST	P12954 saccharomyc
28	87.5	6.9	1813	1 UN13_CAREL	P27715 caenorhabdi
29	87	6.9	664	1 ZAAA_CAREL	Q09543 caenorhabdi
30	86.5	6.9	384	1 NRFF_HABIN	P44942 haemophilus
31	86.5	6.9	2492	1 TALA_DICDI	P54633 dictyostell
32	86	6.8	469	1 C39A_HUMAN	Q9ny15 homo sapien
33	86	6.8	1146	1 KMHA_DICDI	P42557 dictyostell

34	85	6.7	805	1 SUS2_ARATH	Q00917 arabidopsis
35	85	6.7	953	1 UVRA_RICPR	Q9zcc3 rickettsia
36	85	6.7	1188	1 PPSA_METJA	Q57962 methanococc
37	84.5	6.7	466	1 DNAA_PROMT	P22837 proteus mir
38	84.5	6.7	964	1 CAPF_TOBAC	P27154 nicotiana t
39	84.5	6.7	1075	1 PST2_SCHPO	Q13919 schizosacch
40	84.5	6.7	2156	1 RPL_HUMAN	P56715 homo sapien
41	84	6.7	935	1 COBG_YEAST	P32074 saccharomyc
42	84	6.7	935	1 YJ31_YEAST	P40355 saccharomyc
43	84	6.7	1224	1 MGNS_YEAST	P52918 saccharomyc
44	84	6.7	1522	1 BAI3_HUMAN	Q60242 homo sapien
45	83.5	6.6	442	1 MURC_STRPB	Q8p2el streptococc

ALIGNMENTS

RESULT 1
ID SCF_HUMAN STANDARD: PRT: 273 AA.
AC P21583; Q16487; Q9UOK7;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
DE cell growth factor) (MGF).
GN KITLG OR MGF OR SCF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1)
RX MEDLINE=91004219; PubMed=2208279;
RA Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,
RA Morris C.F., McNeice I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,
RA Smith K.A., Johnson M.U., Parker V.P., Flores J.C., Patel A.C.,
RA Fisher E.F., Erivac H.O., Herrera C.J., Wypych J., Sachdev R.K.,
RA Pope J.A., Leslie I., Wen D., Lin C.H., Cupples R.L., Zeebo K.M.,
RT "Primary structure and functional expression of rat and human stem
RT cell factor DNAs."
RL Cell 63:203-211(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2)
RX MEDLINE=9160429; PubMed=10049787;
RA Blair H.C., Julian B.A., Cao X., Jordan S.E., Dong S.S.,
RT "Parathyroid hormone-regulated production of stem cell factor in human
RT osteoblasts and osteoblast-like cells."
RL Biochem. Biophys. Res. Commun. 255:778-784(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Han C., Peng X., Yuan J., Qiang B.,
RN Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 167-248 FROM N.A. (ISOFORM 2).
RX MEDLINE=92360843; PubMed=1379846;
RA Toyota M., Hinoeda Y., Itoh F., Tsujisaki M., Inai K., Yachi A.,
RT "Expression of two types of kit ligand mRNAs in human tumor cells."
RN Int. J. Hematol. 55:301-304(1992).
CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
CC augment the proliferation of both myeloid and lymphoid
CC hematopoietic progenitors in bone marrow culture. Mediates also
CC cell-cell adhesion. Acts synergistically with other cytokines,
CC probably interleukins.
CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
CC Also exists as a secreted soluble form (isoform 1 only) (By
CC similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=SCF248;
CC IsoId=P21583-1; Sequence=Displayed;
CC Name=2; Synonyms=SCF220;

```

CC      IsoId=D21583-2; Sequence=VSP_006022;
CC      DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC      -1- PIM: A soluble form is produced by proteolytic processing of
CC      isoform 1 in the extracellular domain.
CC      -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC      DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC      WWW="http://www.intobio.org.fr/services/chromosome/Genes/MGPID142.html"
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M59964; AAA85450.1; -
DR      EMBL; AF119835; AAD22048.1; -
DR      EMBL; AF400483; AAK92485.1; -
DR      EMBL; AF400437; AAK92486.1; -
DR      EMBL; S42571; AAB22846.2; -
DR      PIR; A35974; A35974.
DR      PIR; B61190; B61190.
DR      Genew; HGNC:6343; KITLG.
DR      MIM; 184745; -
DR      GO; GO:0005173; F:stem cell factor receptor binding activity; TAS.
DR      GO; GO:0008283; P:cell proliferation; TAS.
DR      GO; GO:0007165; P:signal transduction; TAS.
DR      InterPro; IPR003452; SCF.
DR      Pfam; PF02404; SCF.
KW      Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
KW      Alternative splicing.
FT      SIGNAL 1 25
FT      CHAIN 26 273
FT      DOMAIN 26 214
FT      TRANSMEM 215 237
FT      DOMAIN 238 273
FT      DISULFID 29 114
FT      DISULFID 68 163
FT      CARBOHYD 90 90
FT      CARBOHYD 97 97
FT      CARBOHYD 118 118
FT      CARBOHYD 145 145
FT      CARBOHYD 195 195
FT      VARSPPLIC 174 202
FT      FT
FT      FT
FT      CONFLICT 55 55 L -> S (IN REF. 2 AND 3; AAK92486).
FT      CONFLICT 128 128 K -> R (IN REF. 2 AND 3; AAK92486).
FT      CONFLICT 134 134 L -> F (IN REF. 2 AND 3; AAK92486).
SO      SEQUENCE 273 AA; 30898 MW; 19FD362CB59C6607 CRC64;
Query Match 97.5%; Score 1231; DB 1; Length 273;
Best Local Similarity 89.4%; Pred. No. 8 6e-91;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;
QY      1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVQDVTGLVANLEPKDYMILTKYVPG 60
DB      1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVQDVTGLVANLEPKDYMILTKYVPG 60
QY      61 MDVLPBSHCWISSEWVQLSDSLDLDLDFKSNISEGLSNYSIIDKLNYIYDVLVECKENSS 120
DB      61 MDVLPBSHCWISSEWVQLSDSLDLDLDFKSNISEGLSNYSIIDKLNYIYDVLVECKENSS 120
QY      121 KDLKKSPKSPPEPLFTPEEPFRIFNNSIDAFNDPVVASTSDCVVSSNTLSPEKG----- 174
DB      121 KDLKKSPKSPPEPLFTPEEPFRIFNNSIDAFNDPVVASTSDCVVSSNTLSPEKOSRVSVT 180
QY      121 KDLKKSPKSPPEPLFTPEEPFRIFNNSIDAFNDPVVASTSDCVVSSNTLSPEKOSRVSVT 180
DB      121 KDLKKSPKSPPEPLFTPEEPFRIFNNSIDAFNDPVVASTSDCVVSSNTLSPEKOSRVSVT 180
QY      175 -----KAKNPQDSSILHMAAVALPALFSLIIGFAPGALYMKKR 212
DB      181 KPFMLPVAASSLRNDSSSNRRKAKNPDPDSSILHMAAVALPALFSLIIGFAPGALYMKKR 240
QY      213 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 245

```

```

Db      241 QPSLTRAVENI QINEDNEISMLQEKEREPQEV 273
|||||
RESULT 2
ID SCF_HORSE STANDARD: PRT: 274 AA.
AC 095MD2: 062765; 095MG7: 095MG6; 09N1Y5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
DE cell growth factor) (MGF).
GN KITLG OR MGF OR SCF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxId=9796;
[1]
RN RN
RP SEQUENCE OF 4-264 FROM N.A.
RA Terry R.R., Mickelson J.R., Schmutz S., Cochran E.G., Bailey E.;
RT "Equus caballus mast cell growth factor (MGF).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[2]
RN RN
RP SEQUENCE OF 12-267 FROM N.A.
RA TISSUE=Skin;
RC Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.;
RT "An Equine sequence homologous to stem cell factor (KIT-ligand).";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
[3]
RN RN
RP SEQUENCE OF 107-202 AND 227-274 FROM N.A.
RA Terry R.R., Bailey E.F., Cochran E.G.;
RT "Evaluation of MGF as the candidate gene for Appaloosa spotting.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
[4]
RN RN
RP SEQUENCE OF 147-197 FROM N.A.
RA Caetano A.R., Shine Y.-L., Lyons L.A., Laughlin T.F., O'Brien S.J.,
RA Murray J.D., Bowling A.T.;
RT "A primary Human-Horse comparative gene map.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC CC
CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
augment the proliferation of both myeloid and lymphoid
hematopoietic progenitors in bone marrow culture. Mediates also
cell-cell adhesion. Acts synergistically with other cytokines,
CC CC
CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC CC
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
secreted soluble form (By similarity).
CC CC
CC -1- PIM: A soluble form is produced by proteolytic processing of
the extracellular domain (By similarity).
CC CC
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
-----
CC CC
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entities requires a license agreement (See http://www.ebi.ac.uk/announcements
or send an email to license@sb-sib.ch).
-----
CC CC
CC EMBL: AF401625; AAK94474.1; -
DR EMBL: AF053498; AAC97076.1; -
DR EMBL: AF367704; AAK63249.1; -
DR EMBL: AF367706; AAK63250.1; -
DR EMBL: AF130770; AAK63716.1; -
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF. 1.
KM Growth factor; Glycoprotein; Transmembrane; signal; Cell adhesion.
FT SIGNAL 1 25
FT CHAIN 26 274
FT DOMAIN 26 215
FT TRANSMEM 216 238
FT DOMAIN 239 274
CYTOPLASMIC (POTENTIAL).

```

FT	DISULFID	29	114	BY SIMILARITY.
FT <td>DISULFID</td> <td>68</td> <td>164</td> <td>N-LINKED (GLCNAC. . .)</td>	DISULFID	68	164	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	90	90	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	97	97	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	145	145	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	196	196	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	207	207	N-LINKED (GLCNAC. . .)
FT	CONFLICT	15	15	Q -> P (IN REF. 2).
FT	CONFLICT	241	241	MISSING (IN REF. 3).
SO	SEQUENCE	274 AA:	31217 MW;	96C1D4C9059132F2 CRC64;
Query Match		83.5%;	Score 1053.5;	DB 1; Length 274;
Best local Similarity		76.6%;	Pred. No. 1.1e-76;	
Matches		210;	Conservative 19;	Mismatches 16; Indels 29; Gaps 2
OY	1	1	1	1
DB	1	1	1	1
OY	61	61	61	61
DB	61	61	61	61
OY	121	121	121	121
DB	121	121	121	121
OY	175	175	175	175
DB	181	181	181	181
OY	212	212	212	212
DB	241	241	241	241
RESULT 3				
ID	SCF_FELCA	STANDARD;	PRT;	274 AA.
AC	P79169;			
DT	28-FEB-2003	(Rel. 41, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Kit 1 ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).			
GN	KITLG OR SCF.			
OS	Felis silvestris catus (Cat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.			
OX	NCBI_TaxId=9685;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RX	MEDLINE=97069946; PubMed=8912926;			
RA	Dunham S.P., Onions D.E.;			
RT	"The cloning and sequencing of cDNAs encoding two isoforms of feline stem cell factor.";			
RL	DNA Seq. 6:233-237(1996).			
CC	-I- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).			
CC	-I- SUBUNIT: Homodimer, non-covalently linked (probable).			
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2). Also exists as a secreted soluble form (isoform 1 only) (By similarity).			
CC	-I- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=2;			
CC	Name=1;			
CC	Name=2;			
CC	isoId=P79169-2; Sequence=VSP_006021.			
CC	-I- PTM: A soluble form is produced by proteolytic processing of			

isoform 1 in the extracellular domain (By similarity).

-1- SIMILARITY: BELONGS TO THE SCF FAMILY.

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CC EMBL: D50833; BAA09445.1; -.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF; 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
KW Alternative splicing.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 274 KIT LIGAND.
FT DOMAIN 26 215 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 216 238 POTENTIAL.
FT DOMAIN 239 274 CYTOPLASMIC (POTENTIAL).
FT DISULFID 29 114 BY SIMILARITY.
FT CARBOHYD 68 164 BY SIMILARITY.
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 175 203 DSRVSVTKPFPMALPVAASSLRNDDSSSNR -> G (in isoform 2).
FT /FTid=VSP_006021.
FT /FTid=BDB4791237BE CRC64;

SEQUENCE 274 AA: 30987 MW: CGB7BDB4791237BE CRC64;

Query Match 83.3%; Score 1051.5; DB 1; Length 274;
Best Local Similarity 76.6%; Pred. No. 1.6e-76;
Matches 210; Conservative 17; Mismatches 18; Indels 29; Gaps 2

QY 1 MKKTQTMILITCIYQLILFNPVLTETGICRRNRVNNVADYTKLVANLEKDYMITLKYVG 60
DB 1 MKKTQTMIVTCIYQLILFNPVLTETGICRRNRVTDVADYTKLVANLEKDYMITLKYVG 60
QY 61 MDVLPSCWMSSENVVQSDSLTDLIDKPSNISEGLSNYSIIDKLVNIYDDIVECKENSS 120
DB 61 MDVLPSCWMSVWQSVSLTDLIDKPSNISEGLSNYSIIDKLVNIYDDIVECKGHSS 120
QY 121 KDLKSLFKSPPEPLFTPEEPFRINRSIDAEKDFVVASETSDCVVSSSTLSPKSG----- 174
DB 121 ENVKKSSKSPPEPLFTPEEPFRINRSIDAEKDLKLEMAVSKTSECVVSSSTLSPKSDRSVSV 180
QY 175 -----YAKNPGDSSLHMAAMALPALFSLIIGAFGALYMKK 211
DB 181 TKPFWLPPVAASLRNDDSSSNRKATNPIDPSSIQMAVMAALPACPLVIGFAFGAFYWK 240
QY 212 RQSLTRAVENIQINEEDNISMOKERERQEV 245
DB 241 KQPNLTRVENIQINEEDNISMOKERERQEV 274

RESULT 4
SCF_PIG STANDARD; PRT; 274 AA.
ID SCF_PIG
AC Q29030;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
DE KILIG OR MGF.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxId=9823;
RN [1]
RP SEQUENCE FROM N.A.

RC	TX	TISSUE=uterus;	PUBMED=7508758;
RA	Zhang Z., Anthony R.V.;	"Pocline stem cell factor/c-kit ligand: its molecular cloning and localization within the uterus."	
RL	Biol. Reprod. 50:95-102(1994).		
CC	- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).		
CC	- SUBUNIT: Homodimer, non-covalently linked (Probable).		
CC	- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).		
CC	- PIM: A soluble form is produced by proteolytic processing of the extracellular domain (By similarity).		
CC	- SIMILARITY: BELONGS TO THE SCF FAMILY.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sb.ch/announce/ or send an email to license@isb-sb.ch).		
CC	-----		
DR	EMBL, L07786; AA553670.1; -.		
DR	PIR, I46575; I46575.		
DR	InterPro, IPR003452; SCF.		
DR	Pfam, PF02404; SCF, 1.		
KW	Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.		
FT	SIGNAL	1 25	BY SIMILARITY.
FT	CHAIN	26 274	KIT LIGAND.
FT	DOMAIN	26 215	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	216 238	POTENTIAL.
FT	DOMAIN	239 274	CYTOLASMIC (POTENTIAL).
FT	DISULFID	29 114	BY SIMILARITY.
FT	DISULFID	68 164	BY SIMILARITY.
FT	CARBOHYD	90 90	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	97 97	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	145 145	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	196 196	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ	SEQUENCE	274 AA; 3118 MW; FPGC8711AD7BA6A6 CRC64;	
Query Match	82.2%;	Score 1037.5;	DB 1; Length 274;
Best Local Similarity	75.2%;	Pred. No. 2e-75;	
Matches 206;	Conservative 22;	Mismatches 17;	Indels 29; Gaps 2;
OY	1 MKKQTWTLLTCYIYQDLLFNPFLVYKTEGICRRRVYNNVADVTKLVANLPKDYMITLKYPG	60	
Db	1 MKKQTWTLLTCYIYQDLLFNPFLVYKTEGICRRRVYNNVADVTKLVANLPKDYMITLKYPG	60	
OY	61 MDVLPSCWISSENVVQLSDSLTDLDDKFSNISEGSHNSIIDKLVNIYDDLVVECKVENS	120	
Db	61 MDVLPSCWISSENVVQLSDSLTDLDDKFSNISEGSHNSIIDKLVNIYDDLVVECKVENS	120	
OY	121 KDLKVSFKSPSPRLFTPEEFRIENRSIDAFKDF-VASSETSDCVSSTLSPEKG----	174	
Db	121 ENVKSSKSPSPRLFTPEEFRIENRSIDAFKDF-VASSETSDCVSSTLSPEKG----	180	
OY	175 -----KAKNPGGSSLHMAAMALPALFSLTIGAFGALYWK	211	
Db	181 TKPMLPVAASSLRNDSSSNRKRKSDSIDESSLOMAAVALPAFFSLVIGAFGALYWK	240	
OY	212 ROPSLTRAVENIQTNEEDNEISMLQEKREPOEV	245	
Db	241 KQPNLRTVENIQTNEEDNEISMLQEKREPOEV	274	
RESULT 5	SCF CAPHI	STANDARD;	PRT; 274 AA.
NC	Q95M19;		

DT	28-FEB-2003 (Rel. 41, Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
DE	Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
GN	Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
OS	Capra hircus (Goat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Kuminantia; Pecora; Bovidae; Bovidae; Caprinae; Capra.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Kuminantia; Pecora; Bovidae; Bovidae; Caprinae; Capra.
OX	NCBI_TaxID=9925;
OX	NCBI_TaxID=9925;
RP	SEQUENCE FROM N.A.
RC	STRAIN=Shiba; TISSUE=Brain;
RA	Yanagisawa N., Tanaka S., Yamanouchi K., Tojo H., Tachi C.;
RT	Identification of splicing isoforms of caprine stem cell factor (SCF) transcripts and expression patterns of the two major isoforms, gSCF825 and gSCF741, in the brain and the skin of adult and fetal Shiba goats, Capra hircus."
RL	Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC	-1- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediators also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).
CC	-1- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).
CC	-1- PTM: A soluble form is produced by proteolytic processing of the extracellular domain (By similarity).
CC	-1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC	-----
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CC	-----
DR	EMBL, AB002152; BAB71753.1; -
DR	InterPro, IPR003452; SCF.
DR	Pfam, PF00404; SCF, 1.
KW	Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
FT	CHAIN 1 25
FT	SIGNAL 1 25
FT	DOMAIN 26 274
FT	TRANSSEM 216 238
FT	DOMAIN 239 274
FT	DISULFID 29 114
FT	DISULFID 68 164
FT	CARBOHYD 90 90
FT	CARBOHYD 97 97
FT	CARBOHYD 145 145
FT	CARBOHYD 196 196
SQ	SEQUENCE 274 AA; 31052 MW; BBE669A509EF65D CRC64;
Query March	80.9%; Score 1021.5; DB 1; Length 274;
Best local Similarity	74.5%; Pred. No. 3.8e-74;
Matches 204; Conservative	20; Mismatches 21; Indels 29; Gaps 2
QY	1 MKKTQWTILTCIYQLLLFNPVLVTEGICRRNRVNNVADVTKLVANLPKDYMITLKYVPG 60
DB	1 MKKTQWTILTCIYQLLLFNPVLVSHSGICRRNRVVDVADVTKLVANLPKDYMITLKYVPG 60
QY	61 MDVLPSCWISSENVVQLSDSLTDLLDKFSNISSEGLSNYSITDKLVNYVDLVCEYKENS 120
DB	61 MDVLPSCWISSENVVQLSDSLTDLLDKFSNISSEGLSNYSITDKLVNYVDLVCEYKENS 120
QY	121 KKKSKFSKSEPRFLFTEEPFRINRSIDAFKDE-VVASETSDCVASSTLSPEKG----- 174
DB	121 ENVAKSKSEPRFOTPEKFFGIFPKNSIDAFKDEIVAASTMSSECVISTSTSPEDKSRVSV 180

QY 175 -----KAKNPPGSSSLHMAAMALPALFSLIIGFAGALYWK 211
DB 181 TKPFMLPVAASLSLRNDSSSNRKASNSIEDSLQMAAVALPAFPFLVIGFAGALYWK 240
QY 212 ROPSLTRAVENIQINEEDNEISMLQEKERPEFV 245
DB 241 KQPNLTRVENVQINEEDNEISMLQEKERPEFV 274

RESULT 6
SCF_BOVIN
ID SCF_BOVIN STANDARD; PRT; 274 AA.
AC Q28132; Q9TU74;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE kit ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast
DE cell growth factor) (MGF).
GN KITLG OR SCF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Spleen;
RX MEDLINE=9439176; PubMed=7520283;
RA Zhou J., Hikono H., Ohtaki M., Kubota T., Sakurai M.;
RA "Cloning and characterization of cDNAs encoding two normal isoforms of
RT bovine stem cell factor.";
RL Biochim. Biophys. Acta 1223:148-150(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Fetal brain;
RA Kudo T.;
RT "Bovine counterpart of stem cell factor.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 204-239 FROM N.A., AND VARIANT ASP-218.
RC STRAIN=Belgian Blue;
RX MEDLINE=9931531; PubMed=10384045;
RA Seitz J.J., Schmutz S.M., Thue T.D., Buchanan F.C.;
RA "A missense mutation in the bovine MGF gene is associated with the
RT roan phenotype in Belgian Blue and Shorthorn cattle.";
RL Mamm. Genome 10:710-712(1999).
CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
CC augment the proliferation of both myeloid and lymphoid
CC hematopoietic progenitors in bone marrow culture. Mediates also
CC cell-cell adhesion. Acts synergistically with other cytokines,
CC probably interleukins (By similarity).
CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
CC Also exists as a secreted soluble form (isoform 1 only) (By
CC similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q28132-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q28132-2; Sequence=VSP 006020;
CC -1- PTM: A soluble form is produced by proteolytic processing of
CC isoform 1 in the extracellular domain (By similarity).
CC -1- POLYMORPHISM: The roan locus is responsible for the coat
CC coloration of Belgian Blue and Shorthorn cattle. The solid-colored
CC and white animals are homozygotes, and the roan animals, with
CC intermingled colored and white hairs, are heterozygous. The roan
CC phenotype is due to the Asp-218 mutation.
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC
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DR EMBL; D28934; BAA06061.1; -
DR EMBL; AB033716; BAA94808.1; -
DR EMBL; AF120154; AAD55355.1; -
DR PIR; S47571; S47571.
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
KW Alternative splicing; Polymorphism.
FT SIGNAL 1 25
FT CHAIN 1 26 274
FT DOMAIN 26 215
FT TRANSMEM 216 238
FT DOMAIN 239 274
FT DISULFID 29 114
FT DISULFID 68 164
FT CARBOHYD 90 90
FT CARBOHYD 145 145
FT CARBOHYD 196 196
FT VARSPLIC 175 203
FT ISOFORM 2).
FT FTID=VSP 006020.
FT FT A -> D (IN ROAN).
SQ SEQUENCE 274 AA; 31014 MW; D6C1DB77B0CB12B CRC64;
Query Match 80.7%; Score 1018.5; DB 1; Length 274;
Best Local Similarity 74.1%; Pred. No. 6.6e-74;
Matches 203; Conservative 20; Mismatches 22; Indels 29; Gaps 2;

QY 1 MKKTQWTLITCYLLQLLFNPLVYKTEGICRRNVTNNKVDYKLVNLPDWTITTKYVG 60
DB 1 MKKTQWTLITCYLLQLLFNPLVHTQGCNKRVIDVDVTKLVANLPKDWITTKYVG 60
QY 61 MOVLSHCWISMWVQVLSLTDLDFKFSNISEGLSNYSIIDKLVNIYDDIVECKENSS 120
DB 61 MOVLSHCWISMWVQVLSLTDLDFKFSNISEGLSNYSIIDKLVNIYDDIVECKENSS 120
QY 121 KDLKSKFSPPEPRFLTPPEPFRRIFNRSIDAFKDF-VVASSETSDCVSSTLSPEKG----- 174
DB 121 EHWKSSSPPEPRQTPPEPFRRIFNRSIDAFKDFIVASKNSCEVTSSTSPKOSRSV 180
QY 175 -----KAKNPPGSSSLHMAAMALPALFSLIIGFAGALYWK 211
DB 181 TKPFMLPVAASLSLRNDSSSNRKASNSIEDSLQMAAVALPAFPFLVIGFAGALYWK 240
QY 212 ROPSLTRAVENIQINEEDNEISMLQEKERPEFV 245
DB 241 KQPNLTRVENVQINEEDNEISMLQEKERPEFV 274

RESULT 7
SCF_CANFA
ID SCF_CANFA STANDARD; PRT; 274 AA.
AC Q06220; Q8SPM6;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE kit ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast
DE cell growth factor) (MGF).
GN KITLG OR MGF.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=F-cell;
RX MEDLINE=93106145; PubMed=1281786;
RA Shull R.M., Suggs S.V., Langley K.E., Okino K.H., Jacobsen F.W.,

RA	Martin F.H.;
RT	"Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic progenitors in long-term canine marrow culture.";
RL	Exp. Hematol. 20:1118-1124(1992).
RN	[2]
RP	SEQUENCE OF 17-274 FROM N.A.
RC	TISSUE=tail;
RA	Schmutz S.M., Berryere T.G.;
RT	"MGE sequencing in the dog aids in mapping to CPAL5.";
RL	Submitted (Apr-2002) to the EMBL/Genebank/DBJ databases.
CC	- FUNCTION: Stimulates the proliferation of mast cells; Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins.
CC	- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC	- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form.
CC	- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC	- PTM: A soluble form is produced by proteolytic processing of the extracellular domain (by similarity).
CC	- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC	-----
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CC	-----
DR	EMBL; S53329; AAA24619.1; .-
DR	EMBL; AY094361; AAM16280.1; .-
DR	PIR; I46929; I46929.
DR	InterPro; IPRO03452; SCF.
Pfam; PF02404; SCF; 1.	
KW	Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
FT	SIGNAL 1 25 BY SIMILARITY.
FT	CHAIN 26 274 KIT LIGAND.
FT	DOMAIN 26 215 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 216 238 POTENTIAL.
FT	DOMAIN 239 274 CYTOPLASMIC (POTENTIAL).
FT	DISULFD 29 114 BY SIMILARITY.
FT	DISEULFD 68 164 BY SIMILARITY.
FT	CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE 274 AA; 30869 MW; 4182BB9AED00793B CRC64;
Query Match	80.4%; Score 1014.5; DB 1; Length 274;
Best Local Similarity	74.8%; Pred. No. 1.4e-73;
Matches 205; Conservative 17; Mismatches 23; Indels 29; Gaps 2;	
OY	1 MKKTQTWLTCTCIYIQLLFNLVLTKEGICRRKRVNNVNDYTKLVANLPKDYMITLKYPVG 60 : 1 MKKTQWTIIITTIYIQLLLFNPLVKTKGICGRKVIDVDVDTKLVAANLPKDYLIALKYVPG 60
Db	
OY	61 MDVLPSSHCHWISSEMYVQSDSLTDLLDKPSNTSEGHSNYSIIDKLVNYVDLVECVKENSS 120 : 61 MDVLPSSHCHWISVMWEQSLSLTDLDDKRSNISSEGLSNYSIIDKLVKYIVDDLVECTEGYSF 120
Db	
OY	121 KDLKSPKSPBPRLFTPEEPFRIFNRSIDAKDFP-VVASSETSDCVSVSTSPKSG----- 174 : 121 ENVKKAPSPELRLFTPEEPFRIFNRSIDAKDFLETVASKSSECVSVSTSPKDSRVSV 180
Db	
OY	175 -----KAKNPGGSSITHMAALPALFSLIIGAFAALTYWK 211 : 181 TKPMLDPVAASSLRNDSSSNRKASNSIGDSNIQMAMALPAFFSVIGAFALTYWK 240
Db	
OY	212 RQSLTRAVENIQINEEDNEISMIOEKREEROEV 245 : 241 KQPNLTRVENIQINEEDNEISMIOEKREEROEV 274
Db	

```

RESULT 8
SCF MUSVI
ID SCF MUSVI STANDARD; PRT; 274 AA.
AC Q95N18; Q95NM5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cell ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
cell growth factor) (MGF).
GN KITLG_OR_SCF.
OS Muscula vlsn (American mink).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=9667;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Bennett R.D., Murphy B.D.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Stimulates the proliferation of mast cells. Able to
CC augment the proliferation of both myeloid and lymphoid
CC hematopoietic progenitors in bone marrow culture. Mediates also
CC cell-cell adhesion. Acts synergistically with other cytokines,
CC probably interleukins (By similarity).
CC -I- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
CC secreted soluble form (By similarity).
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q95N18-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q95N18-2; Sequence=VSP_006024;
CC -I- PWM: A soluble form is produced by proteolytic processing of
CC isoform 1 in the extracellular domain (By similarity).
CC -I- SIMILARITY: BELONGS TO THE SCF FAMILY.
-----
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-----
DR EMBL; AY013712; AACG7434.1; -.
DR EMBL; AF323757; AAK73366.1; -.
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
KW Alternative splicing.
KM SIGNAL
FT 1 25
FT CHAIN 26 274
FT DOMAIN 26 215
FT TRANSMEM 216 238
FT DOMAIN 239 274
FT DISULFID 29 114
FT DISULFID 68 164
FT CARBOHYD 90 90
FT CARBOHYD 97 97
FT CARBOHYD 145 145
FT CARBOHYD 196 196
FT VARSPIC 175 203
FT
FT CONFLICT 65 65
FT CONFLICT 171 171
FT CONFLICT 268 274
FT
SEQUENCE 274 AA; 31034 MW; SACL619014AA5E72 CRC64;
1; AAK73366)

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Query Match 80.4%; Score 1014.5; DB 1; Length 274;
 Best Local Similarity 73.7%; Pred. No. 1.4e-73;
 Matches 202; Conservative 20; Mismatches 23; Indels 29; Gaps 2;

QY 1 MKKTQWITTCIYQLLLFNPLVKTGICRRVYNNVQVTKLVANLPKDWITLKYVVG 60
 DB 1 MKKTQWITTCIYQLLLFNPLVKTGICRRVYNNVQVTKLVANLPKDWITLKYVVG 60
 QY 61 MDVLSHCWISPMVAVQLSDSLTDLDFKSNISSEGLSNYSIIDKLVINIVDVLVECVKENS 120
 DB 61 MDVLSHCWISPMVAVQLSDSLTDLDFKSNISSEGLSNYSIIDKLVINIVDVLVECVKENS 120
 QY 121 KDLKTSFKSPERPLFTPEEFRIENRSIDAFKDF-VVASSETDCVVSSTLSEPKG----- 174
 DB 121 EAVKSPKRPFRHFAPEDFPIFNRSIDALDLEVAKTSCEVLPSTLSEPKSRVSV 180
 QY 175 -----KAKNPQDSSLHMAVALPALFSLITGPAFGALYMKK 211
 DB 181 TRPFMLPVVAASSLRNDSSSNRKANPLGDSNLCWAAVALPAFFSLVIGFAGALYMKK 240
 QY 212 ROPSLTRAVENTIQINEEDNEISMLOKEREPOEV 245
 DB 241 KQPNLTRIAENIQINEEDNEISMLOKEREPOEV 274

RESULT 9
 SCF_RAT STANDARD; PRT; 273 AA.
 ID P21581; Q9GMZ4; Q9Z2E7;
 AC 01-MAY-1991 (Rel. 18, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Kit ligand precursor (C-kit ligand) (stem cell) factor (SCF) (mast cell growth factor) (MGF) (hematopoietic growth factor KL).
 GN KITLG OR MGF.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1] Taxid=10116;
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RA Teramoto T., Nagashima M., Thorngeltrson S.S.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-201 FROM N.A., AND PARTIAL SEQUENCE.
 RA MEDLINE=91004219; PubMed=2208279;
 RA Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,
 RA Morris C.F., McNiece I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,
 RA Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,
 RA Fisher E.F., Erjavec H.O., Herrera C.J., Wypych J., Sachdev R.K.,
 RA Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zeebo K.M.;
 RT "Primary structure and functional expression of rat and human stem cell factor DNAs".
 RT Cell 63:203-211(1990).
 RN [3]
 RP SEQUENCE OF 26-190. CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RC STRAIN=Buffalo; TISSUE=Liver;
 RX MEDLINE=91217037; PubMed=1708771;
 RA Lu H.S., Clagston C.L., Wypych J., Fausset P.R., Lauren S.,
 RA Mendiaz E.A., Zeebo K.M., Langley K.E.;
 RT "Amino acid sequence and post-translational modification of stem cell factor isolated from buffalo rat liver cell-conditioned medium".
 RT J. Biol. Chem. 266:8102-8107(1991).
 RN [4]
 RP SEQUENCE OF 26-39.
 RX MEDLINE=91004218; PubMed=2208278;
 RA Zeebo K.M., Wypych J., McNiece I.K., Lu H.S., Smith K.A.,
 RA Karkare S.B., Sachdev R.K., Yushenko V.N., Birkett N.C.,
 RA Williams L.R., Satyaag V.N., Tung W., Bosseman R.A., Mendiaz E.A.,
 RA Langley K.E.;
 RT "Identification, purification, and biological characterization of RT hematopoietic stem cell factor from buffalo rat liver-conditioned medium".

RL Cell 63:195-201(1990).
 CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
 CC augment the proliferation of both myeloid and lymphoid
 CC hematopoietic progenitors in bone marrow culture. Mediates also
 CC cell-cell adhesion. Acts synergistically with other cytokines,
 CC probably interleukins.
 CC -1- SUBUNIT: Homodimer, non-covalently linked (probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
 CC Also exists as a secreted soluble form (isoform 1 only) (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=KL-1;
 CC IsoId=P21581-1; Sequence=Displayed;
 CC Name=2; Synonyms=KL-2;
 CC IsoId=P21581-2; Sequence=VSP_006025;
 CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -1- PTM: A soluble form is produced by proteolytic processing of
 CC isoform 1 in the extracellular domain.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF071204; AAD02827.1; -
 CC EMBL; AF071205; AAD02828.1; -
 CC EMBL; M59966; AAA42117.1; -
 CC PIR; B35974; B35974; -
 CC InterPro; IPR003452; SCF.
 CC Pfam; PF02404; SCF; 1.
 CC Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
 CC Alternative splicing; Pyroliidone carboxylic acid.
 CC SIGNAL 1 25
 CC CHAIN 26 273
 CC DOMAIN 26 214 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 215 237 POTENTIAL.
 CC CYTOPLASMIC (POTENTIAL).
 CC MOD RES 26 26 PYROLIDONE CARBOXYLIC ACID.
 CC DISULFID 29 114
 CC DISULFID 68 163
 CC CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (PARTIAL).
 CC CARBOHYD 145 145 N-LINKED (GLCNAC. . .).
 CC CARBOHYD 167 167 O-LINKED (PROBABLE).
 CC CARBOHYD 168 168 O-LINKED (PROBABLE).
 CC CARBOHYD 180 180 O-LINKED (PROBABLE).
 CC CARBOHYD 185 195 N-LINKED (GLCNAC. . .) (PARTIAL).
 CC VARSPLIC 174 202 DSRVSVTRPFMLPVVAASSLRNDSSSNR -> G (in
 CC isoform 2).
 CC /FTId=VSP_006025.
 CC S -> P (IN REF. 1; AAD02828).
 CC CONFLICT 207 207 S -> P (IN REF. 1; AAD02828).
 CC SEQ 273 AA; 30712 MW; C0F56527DC3FD27 CRC64;

Query Match 78.6%; Score 992; DB 1; Length 273;
 Best Local Similarity 71.8%; Pred. No. 8.4e-72;
 Matches 196; Conservative 18; Mismatches 31; Indels 28; Gaps 1;

QY 1 MKKTQWITTCIYQLLLFNPLVKTGICRRVYNNVQVTKLVANLPKDWITLKYVVG 60
 DB 1 MKKTQWITTCIYQLLLFNPLVKTGICRRVYNNVQVTKLVANLPKDWITLKYVVG 60
 QY 61 MDVLSHCWISPMVAVQLSDSLTDLDFKSNISSEGLSNYSIIDKLVINIVDVLVECVKENS 120
 DB 61 MDVLSHCWISPMVAVQLSDSLTDLDFKSNISSEGLSNYSIIDKLVINIVDVLVECVKENS 120
 QY 121 KDLKTSFKSPERPLFTPEEFRIENRSIDAFKDFVVASSETDCVVSSTLSEPKG----- 174
 DB 121 KVKESLKKPFRTRNFTPEEFRIENRSIDAFKDFVVASSETDCVVSSTLSEPKSRVSVT 180

OY 175 -----KAKNPPGDSLSHMAALPALFSLIIGFAGALYMKR 212
 DB 181 KPFMLPVAASSLRNDSSSSNRKAASPEDPGIQTWMLPALISIVIGFALCALYMKK 240
 OY 213 QPSLTPRAVENIQINEDNEISMLOEKEREPQEV 245
 DB 241 OSSLTPRAVENIQINEDNEISMLOEKEREPQEV 273
 RESULT 10
 SCF_MOUSE STANDARD; PRT; 273 AA.
 ID SCF_MOUSE P20826; Q62524; Q6222; Q921NS;
 AC G1-FEB-1991 (Rel. 17, Created)
 DT G1-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Klt ligand precursor (C-Klt ligand) (stem cell factor) (SCF) (Maat
 cell ligand factor) (MGF) (hematopoietic growth factor KL) (Steel
 factor).
 GN KITLG OR KITL OR MGF OR SL OR SLF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=WC6F1.
 RX MEDLINE=91004223; PubMed=1698556;
 RA Anderson D.M., Lyman S.D., Baird A., Wignall J.M., Eisenman J.,
 RA Rauch C., March C.J., Boswell H.S., Gimpel S.D., Cosman D.,
 RA Williams D.E.;
 RT "Molecular cloning of mast cell growth factor, a hematopoietin that
 RT is active in both membrane bound and soluble forms.";
 RL Cell 63:235-243(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=92330001; PubMed=1378327;
 RA Huang E.J., Nocka K.H., Buck J., Besmer P.;
 RT "Differential expression and processing of two cell associated forms
 RT of the kit-ligand: KL-1 and KL-2.";
 RL Mol. Biol. Cell 3:349-362(1992).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=WC6F1;
 RX MEDLINE=91160046; PubMed=1705866;
 RA Flanagan J.G., Chan D.C., Leder P.;
 RT "Transmembrane form of the kit ligand growth factor is determined by
 RT alternative splicing and is missing in the Slid mutant.";
 RL Cell 64:1025-1035(1991).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=93012940; PubMed=1383087;
 RA Brannan C.L., Bedell M.A., Resnick J.L., Eppig J.J., Handel M.A.,
 RA Williams D.E., Lyman S.D., Donovan P.J., Jenkins N.A.,
 RA Copeland N.G.;
 RT "Developmental abnormalities in Steel^{17H} mice result from a splicing
 RT defect in the steel factor cytoplasmic tail.";
 RL Genes Dev. 6:1832-1842(1992).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J;
 RX MEDLINE=97002551; PubMed=8849898;
 RA Bedell M.A., Copeland N.G., Jenkins N.A.;
 RT "Multiple pathways for Steel regulation suggested by genomic and
 RT sequence analysis of the murine Steel gene.";
 RL Genetics 142:927-934(1996).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS PRO-193 AND SER-207.
 RC STRAIN=C3H/El; TISSUE=Brain;
 RX MEDLINE=97032534; PubMed=8875893;
 RA Graw J., Loetscher J., Neuhäuser-Klaus A., Pretsch W.,
 RA Schmitt-John T.;
 RT "Molecular analysis of two new Steel mutations in mice shows a
 RT transversion or an insertion.";
 RL Mamm. Genome 7:843-846(1996).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS SER-122, PRO-193 AND
 RP SER-207.
 RC STRAIN=102/El x C3H/El;
 RX MEDLINE=98025115; PubMed=9360640;
 RA Graw J., Neuhäuser-Klaus A., Pretsch W.;
 RT "Detection of a point mutation (A to G) in exon 5 of the murine Mgf
 RT gene defines a novel allele at the Steel locus with a weak
 RT phenotype.";
 RL Mutat. Res. 382:75-78(1997).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kanuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombaerts P.,
 RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
 RA Wyszew-Boris A., Yoshida K., Haegawa Y., Kawaji H., Kohzuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT SER-207.
 RX MEDLINE=22388257; PubMed=12477932.
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko I., Marzina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin L.B., Toshynski S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [10]
 RP SEQUENCE OF 1-270 FROM N.A. (ISOFORM 1), AND SEQUENCE OF 26-65.
 RX MEDLINE=91004221; PubMed=1698557;
 RA Huang E., Nocka K., Beiler D.R., Chu T.Y., Buck J., Lahm H.W.,
 RA Wellner D., Leder P., Besmer P.;
 RT "The hematopoietic growth factor KL is encoded by the Sl locus and is
 RT the ligand of the c-kit receptor, the gene product of the W locus.";
 RL Cell 63:225-233(1990).
 RN [11]
 RP SEQUENCE OF 1-201 FROM N.A.
 RX MEDLINE=91004220; PubMed=1698556;
 RA Zeebo K.M., Williams D.A., Geisler E.N., Broudy V.C., Martin F.H.,
 RA Atkins H.L., Hsu R.-Y., Birkett N.C., Okino K.H., Mudrock D.C.,
 RA Jacobsen F.W., Langley K.E., Smith K.A., Takeishi T., Cattalini B.M.,


```

RA  Galli S.J., Suggs S.V.;
RT  "Srem cell factor is encoded at the Sl locus of the mouse and is the
RL  ligand for the c-kit tyrosine kinase receptor.";
RN  Cell 63:213-224(1990).
RP  [12]
RX  MEDLINE=91004216; PubMed=1698554;
RA  Copeland N.G., Gilbert D.J., Cho B.C., Donovan P.J., Jenkins N.A.,
RA  Cosman D., Anderson D., Lyman S.D., Williams D.E.;
RT  "Mast cell growth factor maps near the steel locus on mouse
RL  chromosome 10 and is deleted in a number of steel alleles.";
RN  Cell 63:175-183(1990).
RP  [13]
RX  PARTIAL SEQUENCE OF 26-78.
RA  MEDLINE=91004215; PubMed=1698553;
RA  Williams D.E., Eisenman J., Baird A., Rauch C., van Ness K.,
RA  March C.D., Park I.S., Martin U., Mochizuki D.Y., Boswell H.S.,
RA  Burgess G.S., Cosman D., Lyman S.D.;
RT  "Identification of a ligand for the c-kit proto-oncogene.";
RL  Cell 63:167-174(1990).
CC  -1- FUNCTION: Stimulates the proliferation of mast cells. Able to
CC  augment the proliferation of both myeloid and lymphoid
CC  hematopoietic progenitors in bone marrow culture. Mediates also
CC  cell-cell adhesion. Acts synergistically with other cytokines,
CC  probably interleukins.
CC  -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC  -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
CC  Also exists as a secreted soluble form (isoform 1 only) (By
CC  similarity).
CC  -1- ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=2;
CC  Name=1; Synonyms=Kl-1;
CC  IsoId=P20826-1; Sequence=Displayed;
CC  Name=2; Synonyms=Kl-2;
CC  IsoId=P20826-2; Sequence=VSP 006023;
CC  -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC  -1- PTM: A soluble form is produced by proteolytic processing of
CC  isoform 1 in the extracellular domain.
CC  -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC  -----
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CC  or send an email to license@sib-sib.ch).
CC  -----
DR  EMBL, M59915; AAA40095.1; -
DR  EMBL, M57647; AAA39538.1; -
DR  EMBL, S40534; AAB22555.2; -
DR  EMBL, X68989; CAA48778.1; -
DR  EMBL, U44724; -; NOT ANNOTATED_CDS.
DR  EMBL, U44725; AAC52447.1; -
DR  EMBL, X95381; CAA64667.1; -
DR  EMBL, X99322; CAA67698.1; -
DR  EMBL, Y10287; CAA71329.1; -
DR  EMBL, AK018777; BAB31402.1; -
DR  EMBL, BC011322; AAA11322.1; -
DR  EMBL, S40364; AAB22554.2; -
DR  EMBL, M59912; AAA39539.1; -
DR  PIR, A37934; A37934.
DR  PIR, S65801; S65801.
DR  MGD, MGI:96974; Kiti1.
DR  GO, GO:0016021; C:integral to membrane; IDA.

Query Match 78.5%; Score 991; DB 1; Length 273;
Best Local Similarity 72.2%; Pred. No. 1e-71;
Matches 197; Conservative 19; Mismatches 29; Indels 28; Gaps 1;

1 MKKQDTWLTTCYVYGLLEFNPVVKTEGICRRRVYNNVNDVYKLVANIKPDYITLKYVP 60
1 MKKQDTWLTTCYVYGLLEFNPVVKTEGICRRRVYNNVNDVYKLVANIKPDYITLNTYAG 60

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OY 61 MDVPSHCWISLSEVQVSDSTLTDLLDFNSNISBELSNYSIITDKLVNIYVDLVECKENSS 120
DB 61 MDVPSHCWIRLDWVIQIUSLSTLTLLDFNSISBELSNYSIITDKLGKIVVDLVLCEENAP 120
OY 121 KDLKSKFSKPEPPLFTPEEFRRIFRNSIDAFCQVVASSETSDCVSSTLSPEKG----- 174
DB 121 KNIKESKRPETRSFTPEEFRRIFRNSIDAFCQVVASSETSDCVSSTLSPEKGSRVSVT 180
OY 175 -----KAKNPPGSSLSLHMAALPALFSLITGAFGALYMKKR 212
DB 181 KPFLMPVVAASSLRNDSSSNRKAAPKEDSGQWTLMALPALISLVIGAFGALYMKKK 240
OY 213 QPSLTRAVENIQINEEDNEISMLQEKREPOEV 245
DB 241 QSSLTRAVENIQINEEDNEISMLQEKREPOEV 273

RESULT 11
SCF_SHEEP
ID SCF_SHEEP STANDARD; PRT; 267 AA.
AC P79368; Q28591;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
  cell growth factor) (MGF) (Fragment).
GN KITLG OR SCF
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
CX NCBI_TaxID=9940;
  [1]
RN SEQUENCE OF 8-267 FROM N.A.
RP TISSUE=Ovarian follicle;
RC MEDLINE=96413880; PubMed=8662240;
RA Tisdall D.J., Quirke L.D., Galloway S.M.;
RT "Ovine stem cell factor gene is located within a syntenic group on
  chromosome 3 conserved across mammalian species.";
RL Mamm. Genome 7:472-473 (1996).
  [2]
RN SEQUENCE OF 1-202 FROM N.A.
RP McInnes C.J., Logan M., Falconer V.M., Rawlins P., Huntly J., Haig D.;
RA "Molecular cloning and biological activity of ovine stem cell
  factor.";
RL Submitted (ANG-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Stimulates the proliferation of mast cells. Able to
  augment the proliferation of both myeloid and lymphoid
  hematopoietic progenitors in bone marrow culture. Mediates also
  cell-cell adhesion. Acts synergistically with other cytokines,
  probably interleukins (By similarity).
CC -!- SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
  secreted soluble form (By similarity).
CC -!- PTM: A soluble form is produced by proteolytic processing of
  the extracellular domain (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SCF FAMILY.
-----
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  or send an email to license@ebi.ac.uk).
CC
DR EMBL; U89874; AAB49491.1; -
DR EMBL; Z50743; CAA90620.1; -
DR PIR; S58313; S58313
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.

```

FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 >267 KIT LIGAND.
 FT DOMAIN 26 215 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 216 238 POTENTIAL.
 FT DOMAIN 239 >267 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 29 114 BY SIMILARITY.
 FT DISULFID 68 164 BY SIMILARITY.
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 267 267
 SQ SEQUENCE 267 AA; 30148 MW; 909D959E4B9EC841 CRC64;

Query Match 78.5%; Score 990.5; DB 1; Length 267;
 Best Local Similarity 74.2%; Pred. No. 1.1e-71;
 Matches 198; Conservative 19; Mismatches 21; Indels 29; Gaps 2;

QY 1 MKKTQWILTCIYQLLLFNPLVTEGICRNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
 1 MKKTQWILTCIYQLLLFNPLVTEGICRNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
 DB 1 MKKTQWILTCIYQLLLFNPLVTEGICRNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
 QY 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISGLSNYSIIDLVNIYDDLYECVKENS 120
 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISGLSNYSIIDLVNIYDDLYECVKENS 120
 DB 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISGLSNYSIIDLVNIYDDLYECVKENS 120
 QY 121 KDLKSEKSPPEPLFTPEEFRIENRSIDAFKDF-VVASETSDCVVSSSTLSPKSG- 174
 121 KDLKSEKSPPEPLFTPEEFRIENRSIDAFKDF-VVASETSDCVVSSSTLSPKSG- 174
 DB 121 ENVKSSKSPPEPLFTPEEFRIENRSIDAFKDF-VVASETSDCVVSSSTLSPKSG- 180
 121 ENVKSSKSPPEPLFTPEEFRIENRSIDAFKDF-VVASETSDCVVSSSTLSPKSG- 180
 QY 175 -----KAKNPPGDSLSLHMAAMALPALFSLIIGAFGALYMK 211
 175 -----KAKNPPGDSLSLHMAAMALPALFSLIIGAFGALYMK 211
 DB 181 TRKFMPLPVAAASLRNDSSSNRKAISNIEDSLQWAAVALPAFSLVIGFAPGALYMK 240
 181 TRKFMPLPVAAASLRNDSSSNRKAISNIEDSLQWAAVALPAFSLVIGFAPGALYMK 240
 QY 212 ROPSLTRAVENIQTNEEDNEISMLQEK 238
 212 ROPSLTRAVENIQTNEEDNEISMLQEK 238
 DB 241 KOPNLTTRVENRQINEEDNEISMLQEK 267
 241 KOPNLTTRVENRQINEEDNEISMLQEK 267

RESULT 12
 SCF_CHICK STANDARD; PRT; 287 AA.
 ID SCF_CHICK
 AC Q90108;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
 GN KITLG OR SCF.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Gallus.
 OC NCBI_TaxID=9031;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93273244; PubMed=7684722;
 RA Zhou J., Ohtaki M., Sakurai M.;
 RT "Sequence of a cDNA encoding chicken stem cell factor.";
 RL Gene 127:269-270(1993).
 CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hemopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).
 CC -1- SUBUNIT: Homodimer, non-covalently linked (Probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).
 CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -1- PTM: A soluble form is produced by proteolytic processing of the extracellular domain (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----

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 CC -----
 DR EMBL, D13516; BAA0273.1; -;
 DR PIR, JN0637; JN0637;
 DR InterPro, IPR003452; SCF.
 DR Pfam, PF02404; SCF, 1.
 KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 287 KIT LIGAND.
 FT DOMAIN 26 225 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 226 246 POTENTIAL.
 FT DOMAIN 247 287 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 29 117 BY SIMILARITY.
 FT DISULFID 68 167 BY SIMILARITY.
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 287 AA; 32328 MW; 6AE8556ADC152578 CRC64;

Query Match 46.3%; Score 584; DB 1; Length 287;
 Best Local Similarity 44.6%; Pred. No. 2.3e-39;
 Matches 128; Conservative 46; Mismatches 71; Indels 42; Gaps 7;

QY 1 MKKTQWILTCIYQLLLFNPLVTEGICRNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
 1 MKKTQWILTCIYQLLLFNPLVTEGICRNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
 DB 1 MKKTQWILTCIYQLLLFNPLVTEGICRNRVTNNVKDVKLVANLPKDYMTTLKYVPG 60
 QY 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNI-----SEGLSNYSIIDLVNIYDDLYECVKE 117
 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNI-----SEGLSNYSIIDLVNIYDDLYECVKE 117
 DB 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNI-----SEGLSNYSIIDLVNIYDDLYECVKE 120
 QY 118 NSSKD-LKKSFPSPPEPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSSSTL-SPEKKG 175
 118 NSSKD-LKKSFPSPPEPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSSSTL-SPEKKG 175
 DB 121 DKNDPFIENGHIYEDDFIENPFRLNFTIYVKEFADSLDKNDCTMPSTVEPENS 180
 121 DKNDPFIENGHIYEDDFIENPFRLNFTIYVKEFADSLDKNDCTMPSTVEPENS 180
 QY 176 -----AKNPP-----GSSLHMAAMALPALFSLIIG 201
 176 -----AKNPP-----GSSLHMAAMALPALFSLIIG 201
 DB 181 RVAVTKTSPPVAAASLRNDSSSNRKAISNIEDSLQWAAVALPAFSLVIGFAPGALYMK 240
 181 RVAVTKTSPPVAAASLRNDSSSNRKAISNIEDSLQWAAVALPAFSLVIGFAPGALYMK 240
 QY 202 FAFGLYMKKQRP-SLTRAVENIQN--EENNEISMLQEKREPEV 245
 202 FAFGLYMKKQRP-SLTRAVENIQN--EENNEISMLQEKREPEV 245
 DB 241 FLGALYMKKTHPKSPRESNETIOCHGCEENNEISMLQEKREHLQV 287
 241 FLGALYMKKTHPKSPRESNETIOCHGCEENNEISMLQEKREHLQV 287

RESULT 13
 SCF_COTUJ STANDARD; PRT; 287 AA.
 ID SCF_COTUJ
 AC Q90314; Q90315;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
 GN KITLG OR SCF.
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Coturnix.
 OC NCBI_TaxID=93934;
 RN 11
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=96283808; PubMed=8679698;
 RA Peltite J.N., Kulik M.J.;
 RT "Cloning and characterization of cDNAs encoding two forms of avian stem cell factor.";
 RL Biochim. Biophys. Acta 1307:149-151(1996).
 CC -1- FUNCTION: Stimulates the proliferation of mast cells. Able to

```
CC augment the proliferation of both myeloid and lymphoid
CC hematopoietic progenitors in bone marrow culture. Mediates also
CC cell-cell adhesion. Acts synergistically with other cytokines,
CC probably interleukins (By similarity).
CC SUBUNIT: Homodimer, non-covalently linked (Probable).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
CC Also exists as a secreted soluble form (isoform 1 only) (By
CC similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Name=1;
CC Name=2;
CC IsoId=Q090314-1; Sequence=Displayed;
CC IsoId=Q090314-2; Sequence=VSP 006026;
CC -1- PTM: A soluble form is produced by proteolytic processing of
CC isoform 1 in the extracellular domain.
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U43078; AAC59933.1; -.
CC DR EMBL: U43078; AAC59934.1; -.
CC DR InterPro: IPR003452; SCF.
CC DR Pfam: PF02404; SCF. 1.
CC KM Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion;
CC Alternative splicing.
CC FT SIGNAL 1 25
CC FT CHAIN 26 287
CC FT DOMAIN 26 225
CC FT TRANSMEM 226 246
CC FT DOMAIN 247 287
CC FT DISULFID 29 117
CC FT DISULFID 68 167
CC FT CARBOHYD 100 100
CC FT CARBOHYD 106 106
CC FT CARBOHYD 149 149
CC FT CARBOHYD 178 178
CC FT CARBOHYD 200 200
CC FT CARBOHYD 206 206
CC FT VARSPPLIC 179 213
CC FT
CC FT
CC SQ SEQUENCE 287 AA; 32455 MW; ABA81AER422A702E CRC64;
CC
CC Query Match 46.2%; Score 583; DB 1; Length 287;
CC Best Local Similarity 44.3%; Pred. No. 2. de-39;
CC Matches 127; Conservative 47; Mismatches 71; Indels 42; Gaps 7;
CC
CC 1 MKKTQWIIITCIYQLLLFNPLVTEGICGRNRTNNVKDVTGLVANLPKDYMTLTKVPG 60
CC 1 MKKAQWIIITCIYQLLLFNPLVTEGICGRNRTNNVKDVTGLVANLPKDYMTLTKVPG 60
CC
CC 61 MDVLPSCWISSEWVQVLSLTDLDKFE--SNISEGLSNYSIIIDKLVNIVDDLVCEVKE 117
CC 61 MDVLPSCWISSEWVQVLSLTDLDKFE--SNISEGLSNYSIIIDKLVNIVDDLVCEVKE 117
CC
CC 61 MDVLPSCWISSEWVQVLSLTDLDKFE--SNISEGLSNYSIIIDKLVNIVDDLVCEVKE 117
CC 61 MDVLPSCWISSEWVQVLSLTDLDKFE--SNISEGLSNYSIIIDKLVNIVDDLVCEVKE 117
CC
CC 118 NSSKD-LKSKFSKSEPPFLTPPEEFRIFNRSIDAFKDFVAVASSTDCVSSITL-SPKPK 175
CC 118 NSSKD-LKSKFSKSEPPFLTPPEEFRIFNRSIDAFKDFVAVASSTDCVSSITL-SPKPK 175
CC
CC 121 DKNDPFIKENGHLYEEDRFIPENFFRLNRTIEVYKFAOSLDPKNDIMPSYVETPEPND 180
CC 121 DKNDPFIKENGHLYEEDRFIPENFFRLNRTIEVYKFAOSLDPKNDIMPSYVETPEPND 180
CC
CC 176 -----AKPP-----GDSSLHWMAALPALFSLIIG 201
CC 176 -----AKPP-----GDSSLHWMAALPALFSLIIG 201
CC
CC 181 RVAVTKTISFPVVAASLRDSDSGSNSSNKALGFISSSSLQGISLTLSTLSLIG 240
CC 181 RVAVTKTISFPVVAASLRDSDSGSNSSNKALGFISSSSLQGISLTLSTLSLIG 240
CC
CC 202 FAFGALYWKGRQP-SLTRAVENIQT--EEDNEISMLQEKEREFOEV 245
CC 202 FAFGALYWKGRQP-SLTRAVENIQT--EEDNEISMLQEKEREFOEV 245
CC
CC 241 FILGVIVYKTKTHPKRPSNSNETTQCHCGQENEISMLQEKEREFOEV 287
CC 241 FILGVIVYKTKTHPKRPSNSNETTQCHCGQENEISMLQEKEREFOEV 287
CC
CC Db
```

```
RESULT 14
MURE_WIGBR
ID MURE_WIGBR STANDARD; PRT; 496 AA.
AC Q8D2Z1;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE UDP-N-acetylmuramoyl-L-D-glutamate--2,6-diaminopimelate ligase
DE (EC 6.3.2.13) (UDP-N-acetylmuramyl-tripeptide synthetase) (Meso-
DE diaminopimelate-adding enzyme) (UDP-MurNac-tripeptide synthetase).
GN MURE OR WIGBR2110.
OS Wigglesworthia glossinidia brevipalpis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Wigglesworthia.
OX NCBI_TaxId=36870;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22297718; PubMed=12219091;
RA Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
RA Aksoy S.;
RT Genome sequence of the endocellular obligate symbiont of tsetse
RT flies, Wigglesworthia glossinidia.
RL Nat. Genet. 32:402-407(2002).
CC -1- FUNCTION: Cell wall formation. Diaminopimelic acid adding enzyme
CC (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl-L-alanyl-D-
CC glutamate + meso-2,6-diaminohexanoate = ADP + phosphate + UDP-
CC N-acetylmuramoyl-L-alanyl-D-gamma-glutamyl-meso-2,6-diamino-
CC heptanedioate.
CC -1- PATHWAY: Peptidoglycan biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the murCER family.
CC -----
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CC -----
CC EMBL: AB063521; BAC24357.1; -.
CC DR HAMM, MF 00208; 1.
CC DR InterPro: IPR005761; Mure.
CC DR InterPro: IPR000713; Mur_ligase.
CC DR InterPro: IPR004101; Mur_ligase_C.
CC DR Pfam: PF01225; Mur_ligase; 1.
CC DR Pfam: PF02875; Mur_ligase_C; 1.
CC DR TIGRfam: TIGR01085; mure; 1.
CC KM Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
CC NP-binding; Complete proteome.
CC FT BIND 118 124
CC FT ATP (POTENTIAL).
CC SQ SEQUENCE 496 AA; 57220 MW; AB624DA57ADDAC1B CRC64;
CC
CC Query Match 7.8%; Score 99; DB 1; Length 496;
CC Best Local Similarity 21.2%; Pred. No. 1.5;
CC Matches 50; Conservative 44; Mismatches 78; Indels 64; Gaps 12;
CC
CC 1 MKKTQWIIITCIYQLLLFNPLVTEGICGRNRTNNVKDVTGLVANLPKDYMTLTKVPG 50
CC 1 MKKSQTNTSALIKCQLLNFPLKKNINIVMEVSSGHQNNV-NINFFSAIFSLSD 212
CC
CC 51 YMTLLKYVGMVPLPSHCWISSEWVQVLSLTDLDKFSNISEGLSNY-SITDK-LVNI 107
CC 51 YMTLLKYVGMVPLPSHCWISSEWVQVLSLTDLDKFSNISEGLSNY-SITDK-LVNI 107
CC
CC 213 -----HIDYHKNMQYEQSKKFLSKL-NVYKYLINVDVIGKMWIKKI 255
CC 213 -----HIDYHKNMQYEQSKKFLSKL-NVYKYLINVDVIGKMWIKKI 255
CC
CC 108 VDDLVCEVENSCKLAKSKFSPERPLTPPEEFRIFNRSIDAFKDFVAVASSTDCVSS 167
CC 108 VDDLVCEVENSCKLAKSKFSPERPLTPPEEFRIFNRSIDAFKDFVAVASSTDCVSS 167
CC
CC 256 PMSIIVSTKSKSIKKFKNL-----KMYVKDIFPHYFGTKLS-----ISSWGSCVINT 303
CC 256 PMSIIVSTKSKSIKKFKNL-----KMYVKDIFPHYFGTKLS-----ISSWGSCVINT 303
CC
CC Db
```

DB 304 KIF-----GFFNNLLSPVAL--LTIGYF-----KSLANVAENL 338

RESULT 15

ID T2EA_YEAST STANDARD; PRT; 482 AA.

AC F36100;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Transcription initiation factor IIE, alpha subunit (TFII α)

DE (transcription factor A large subunit) (Factor A 66 kDa subunit).

GN TPA1 OR YKL028W.

OS Saccharomyces cerevisiae (Baker's Yeast).

OC Burkholderia; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 66-71; 102-108 AND 206-220.

RC STRAIN=B926;

RX MEDLINE=95050500; PubMed=7961670;

RA Feaver W.J., Henry N.L., Bushnell D.A., Sayre M.H., Brickner J.H.,

RT Gileadi O., Kornberg R.D.;

RT "Yeast TFII α . Cloning, expression, and homology to vertebrate

RT proteins.";

RL J. Biol. Chem. 269:27549-27553 (1994).

RN [2]

RP SEQUENCE FROM N.A.

RA Rieger M.;

RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: RECRUITS TFIIH TO THE INITIATION COMPLEX AND STIMULATES

CC THE RNA POLYMERASE II C-TERMINAL DOMAIN KINASE AND DNA-DEPENDENT

CC ATPASE ACTIVITIES OF TFIIH. BOTH TFIIH AND TFII α ARE REQUIRED FOR

CC PROMOTER CLEARANCE BY RNA POLYMERASE (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -!- SIMILARITY: BELONGS TO THE TFII α ALPHA SUBUNIT FAMILY.

CC

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CC or send an email to license@sib-sib.ch).

CC

DR EMBL; U12825; AA62665.1; -

DR EMBL; Z28028; CA81863.1; -

DR PIR; S37845; S37845.

DR TRANSFAC; T02239; -

DR SGD; S0001511; TPA1.

DR InterPro; IPR002853; TFII α .

DR Pfam; PF02002; TFII α .

DR SMART; SM00531; TFII α .

DR Transcription regulation; Nuclear protein; Zinc-finger.

DR Transcription regulation; Nuclear protein; Zinc-finger.

FT ZN FING 124 152 C4-TYPE (POTENTIAL).

FT DOMAIN 374 482 ASP/GLU-RICH (HIGHLY ACIDIC).

FT FT 374 392 POLY-GLU.

SEQUENCE 482 AA; 54742 MW; 3E789DFC4247EF8A CRC64;

Query Match 7.7%; Score 97; DB 1; Length 482;

Best Local Similarity 18.4%; Pred. No. 2.1;

Matches 54; Conservative 53; Mismatches 89; Indels 98; Gaps 11;

QY 12 IVQLLEPLVKGICGNRVNKKVTKLVANIPKDYMITL----- 55

DB 27 LVLDALIFSHVAEDDL-KQLSINKTEGLPIARLSRDLISIHKOREYPPNSKSVERY 85

QY 56 -----KVPMDVLPSCW--ISEMNVQLSDSLD-----LLDKFSNI----- 91

DB 86 YYYVKKPFAIDAK--WYVHOVORLKDDLKNSSEPNMGWPCICLTXYTQLEAVQLNF 142

QY 92 -----SEGLSNYSIIDKLAVNIIVDLVACV-----KENSCKDLKSKFSKP 130

DB 143 DTEFLCSLCEPVEDESGKKNKEKODKLNRIMDOIQIIDSLSKIDDSRIEENTFEIA 202

QY 131 EPRLLTPEEFRIFFRSIDAFPDVVASETDCVSSSTLSPEKGAKNPPGDSLSHWMAM 190

DB 203 LARLIPQ-----NOSHAAV-----TYNPKGSTMFRPGDQA----- 234

QY 191 ALPALFSLIGFAGALYMKRQPSLTRAVENTIQINEEDNEISMLOEKEREFOE 244

DB 235 PLPNLMGTALGND-----SRAGANSQATYIHINTTASDVAQRELOERQAE 283

Search completed: February 5, 2004, 15:05:52

Job time : 8.76171 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 14:59:08 / Search time 28.6846 Seconds
(Without alignments)
2204.073 Million cell updates/sec

Title: US-09-224-683-63

Perfect score: 1262
Sequence: 1 MKKTQTWITCIYLQLLFN.....NEEDNEISMLQEKEREFGQEV 245

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPTRMBL_23:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	715	56.7	208	11	064384
2	509	40.3	123	11	061854
3	480	38.0	160	11	08C9K1
4	339	26.9	271	13	09YGP2
5	286	22.7	270	13	08AVN7
6	145	11.5	36	6	08SPM7
7	128	10.1	1697	5	08IFW4
8	128	10.1	1711	5	08MWP2
9	128	10.1	1713	5	08MWP1
10	128	10.1	1716	5	08MWP2
11	109	8.6	937	10	09MAL4
12	105.5	8.4	1515	5	08IM40
13	102.5	8.1	919	10	09LPD8
14	102.5	8.1	1498	3	096VK6
15	102.5	8.1	1498	3	09P884
16	102	8.1	1501	3	096VL9

17	99	7.8	496	16	08D2Z1	08d2z1 wigleswort
18	99	7.8	539	12	091H18	091h18 discula des
19	97.5	7.7	402	11	035444	035444 mus musculus
20	97	7.7	1447	16	09POJ8	09pj8 ureaplasma
21	95.5	7.6	1444	5	08ICB9	08icb9 plasmidium
22	94.5	7.5	1515	3	096VK4	096vk4 emericella
23	93.5	7.4	576	11	062970	062970 ratius norv
24	93.5	7.4	647	16	098PP9	098pp9 mycoplasma
25	93.5	7.4	3227	3	013834	013834 schizosach
26	93	7.4	1298	10	09LSA4	09lsa4 arabidopsis
27	93	7.4	1962	10	09FIC2	09fic2 arabidopsis
28	92.5	7.3	335	17	08PXU1	08pxu1 methanosarc
29	92.5	7.3	512	16	09CGA7	09cga7 lactococcus
30	92.5	7.3	534	5	021299	021299 caenorhabdi
31	92	7.3	420	16	098OM8	098om8 mycoplasma
32	92	7.3	821	16	092RE5	092re5 listeria in
33	91.5	7.3	309	16	08UBA3	08uba3 agrobacteri
34	91.5	7.3	1993	5	P90670	P90670 aplysia cal
35	91.5	7.3	2907	5	08IC71	08ic71 plasmidium
36	91	7.2	281	16	08EUV6	08euv6 mycoplasma
37	91	7.2	317	5	09VTY2	09vtv2 drosophila
38	91	7.2	317	5	08SXB8	08sxb8 drosophila
39	90.5	7.2	616	17	026384	026384 methanobact
40	90.5	7.2	774	5	020469	020469 caenorhabdi
41	90.5	7.2	1056	16	08REF7	08ref7 fusobacteri
42	90.5	7.2	1677	12	086W0	086w0 rice tungro
43	90	7.1	273	11	08C6T7	08c6t7 mus musculu
44	90	7.1	464	16	08EQS0	08eqs0 oceanobacil
45	90	7.1	1218	12	08VAV7	08vav7 white spot

ALIGNMENTS

RESULT 1

ID 064384 PRELIMINARY; PRT; 208 AA.

AC 064384;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Mast cell growth factor (Fragment).
GN KITL OR MGF OR SL OR KL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92330001; PubMed=1378327;
RA Huang E.J., Nocka K.H., Buck J., Besmer P.;
RT "Differential expression and processing of two cell associated forms
of the Kit-1 ligand: KL-1 and KL-2".
RL Mol. Biol. Cell 3:349-362(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91160046; PubMed=1705866;
RA Flanagan J.G., Chan D.C., Leder P.;
RT "Transmembrane form of the kit ligand growth factor is determined by
cell alternative splicing and is missing in the Sld mutant".
RL Cell 64:1025-1035(1991).
DR EMBL: 540536; AAA82556.2; -
DR EMBL: M64262; AAA9378.1; -
DR MGD: MGI:96974; Kitl.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF, 1.
FT NON TER 208
SQ SEQUENCE 208 AA; 23222 MW; C7ADD63956EB817 CRC64;

Query Match 56.7%; Score 715; DB 11; Length 208;
Best Local Similarity 79.8%; Pred. No. 3.2e-52;
Matches 138; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

```
QY 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWIMSENVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
DB 61 MDVLPSCWIMSENVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
QY 121 KDILKSKFSPEPRILFTPEEFRIENRSDAFKDFVVASSETSDCVSSTLSPEK 173
DB 121 KNIKESPKRPERTSFTPEEFRIENRSDAFKDFVVASSETSDCVSSTLSPEK 173

RESULT 2
Q61854 PRELIMINARY; PRT; 123 AA.
ID 061854;
AC 061854;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Mast cell growth factor.
GN KITL OR MGF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=97032534; PubMed=8875893;
RA Graw J., Loester J., Neuhauser-Klaus A., Pretsch W., Schmitt-John T.;
RT "Molecular analysis of two new Steel mutations in mice shows a
RT transversion or an insertion."
RL Mamm. Genome 7:843-846 (1996).
DR EMBL: X85379; CAA54666.1; -.
DR MGI: 96974; Kitl.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF; 1.
SQ SEQUENCE 123 AA; 13892 MW; A872B4554A85D642 CRC64;

Query Match
Best Local Similarity 40.3%; Score 509; DB 11; Length 123;
Matches 98; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWIMSENVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
DB 61 MDVLPSCWIMSENVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 120
QY 121 K 121
DB 121 K 121

RESULT 3
Q68C9K1 PRELIMINARY; PRT; 160 AA.
ID 068C9K1;
AC 068C9K1;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Kit ligand (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN 1;
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
```

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RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RA "Analysis of the mouse transcriptome based on functional annotation of
RA 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL: AK041961; BAC31113.1; -.
SQ SEQUENCE 160 AA; 17492 MW; B12AC581346AAE6D CRC64;

Query Match
Best Local Similarity 38.0%; Score 480; DB 11; Length 160;
Matches 92; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 6 TWILTCIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPGMDVLP 65
DB 46 TWILTCIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPGMDVLP 105
QY 66 SHCWIMSENVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 119
DB 106 SHCWIMSENVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVKENS 159

RESULT 4
Q9YGP2 PRELIMINARY; PRT; 271 AA.
ID Q9YGP2;
AC Q9YGP2;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Steel factor.
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OX NCBI_Taxid=8296;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=9929573; PubMed=10370116;
RA Parichy D.M., Stigson M., Voss S.R.;
RT "Genetic analysis of steel and the pg-W/versican-encoding gene Axxp as
RT candidates for the white (d) pigmentation mutant in the salamander
RT Ambystoma mexicanum."
RL Dev. Genes Evol. 209:349-356 (1999).
DR EMBL: AF119044; AAD17253.1; -.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF; 1.
SQ SEQUENCE 271 AA; 30075 MW; 876977ABE7D53EB4 CRC64;

Query Match
Best Local Similarity 26.9%; Score 339; DB 13; Length 271;
Matches 97; Conservative 36; Mismatches 91; Indels 52; Gaps 11;

QY 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVKDVKLVANLPKDYMITLKYVPG 60
QY 57 YVPGMDVLPSCWIMSENVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVK 116
DB 54 YVPGMDVLPSCWIMSENVVQSDSLTDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECVK 110
QY 117 -----ENSKDKKSKFSPEPRILFTPEEFRIENRSDAFK-----DFVASSET- 160
DB 111 SGLDNEFFINDPFDYGE---FVPKKEFKVVTITLLFKAIHMGDDSGELCVTTETP 167
QY 161 -SDCVSSTLSPEK-----GKAKNPG-----DS-----SIHMAAMALPALFSLIGFAF 204
DB 168 LSDLPVGVTKSAFSEFWPSSRRKREGIPNAKPDSTSGLAETPYVALISLSIVLGPFI 227
QY 205 GALYWKRKQPSLTRAVE---NIQINEEDNEISMLQE 237
DB 228 GAVCVMKMKHRESGSGCEPTAPCPVRKEAEQASMLNQ 263
```


RL Mol. Biochem. Parasitol. 121:275-278 (2002).
 DR EMBL, AF420309; AAM47174.1; -
 SQ SEQUENCE 1711 AA; 205236 MW; 254864576A02A5B CRC64;

Query Match 10.1%; Score 128; DB 5; Length 1711;
 Best Local Similarity 21.4%; Pred. No. 0.083;

Matches 52; Conservative 50; Mismatches 85; Indels 56; Gaps 11;

QY 31 NRYTNVNDVTKLVAN-----LPKDYMTLKXVPGM-DVLPSCWISPMV---Q 76
 ID Q8MMW2 PRELIMINARY; PRT; 1713 AA.
 AC Q8MMW2 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Reticulocyte binding protein-like protein 4.
 GN RH4.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NC NCB1_TaxID=5833;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Honduas I/CDC;
 RX MEDLINE=22030722; PubMed=12034462;
 RA Kaneo O., Mu J.-B., Tsunboi T., Su X.-Z., Torii M.;
 RT "Gene structure and expression of a Plasmodium falciparum 220-kDa
 RT protein homologous to the Plasmodium vivax reticulocyte binding
 RT protein.";
 RL Mol. Biochem. Parasitol. 121:275-278 (2002).
 DR EMBL, AF420310; AAM47175.1; -
 SQ SEQUENCE 1713 AA; 205500 MW; AE975734989F495D CRC64;

RESULT 9
 Q8MMW2 PRELIMINARY; PRT; 1713 AA.
 ID Q8MMW2 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Reticulocyte binding protein-like protein 4.
 GN RH4.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NC NCB1_TaxID=5833;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Honduas I/CDC;
 RX MEDLINE=22030722; PubMed=12034462;
 RA Kaneo O., Mu J.-B., Tsunboi T., Su X.-Z., Torii M.;
 RT "Gene structure and expression of a Plasmodium falciparum 220-kDa
 RT protein homologous to the Plasmodium vivax reticulocyte binding
 RT protein.";
 RL Mol. Biochem. Parasitol. 121:275-278 (2002).
 DR EMBL, AF420310; AAM47175.1; -
 SQ SEQUENCE 1713 AA; 205500 MW; AE975734989F495D CRC64;

Query Match 10.1%; Score 128; DB 5; Length 1713;
 Best Local Similarity 21.4%; Pred. No. 0.083;

Matches 52; Conservative 50; Mismatches 85; Indels 56; Gaps 11;

QY 31 NRYTNVNDVTKLVAN-----LPKDYMTLKXVPGM-DVLPSCWISPMV---Q 76
 ID Q8MMW2 PRELIMINARY; PRT; 1713 AA.
 AC Q8MMW2 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Reticulocyte binding protein-like protein 4.
 GN RH4.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NC NCB1_TaxID=5833;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Honduas I/CDC;
 RX MEDLINE=22030722; PubMed=12034462;
 RA Kaneo O., Mu J.-B., Tsunboi T., Su X.-Z., Torii M.;
 RT "Gene structure and expression of a Plasmodium falciparum 220-kDa
 RT protein homologous to the Plasmodium vivax reticulocyte binding
 RT protein.";
 RL Mol. Biochem. Parasitol. 121:275-278 (2002).
 DR EMBL, AF420310; AAM47175.1; -
 SQ SEQUENCE 1713 AA; 205500 MW; AE975734989F495D CRC64;

QY 230 NEI 232
 ID 1448 NEM 1450

RESULT 10

QY 31 NRYTNVNDVTKLVAN-----LPKDYMTLKXVPGM-DVLPSCWISPMV---Q 76
 ID Q8MMW2 PRELIMINARY; PRT; 1716 AA.
 AC Q8MMW2 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Reticulocyte binding protein homolog 4.
 GN RH4.
 OS Plasmodium falciparum (isolate NF54).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NC NCB1_TaxID=5843;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22030722; PubMed=12034462;
 RA Kaneo O., Mu J.-B., Tsunboi T., Su X.-Z., Torii M.;
 RT "Gene structure and expression of a Plasmodium falciparum 220-kDa
 RT protein homologous to the Plasmodium vivax reticulocyte binding
 RT protein.";
 RL Mol. Biochem. Parasitol. 121:275-278 (2002).
 DR EMBL, AF432854; AAM47192.1; -
 SQ SEQUENCE 1716 AA; 205846 MW; 2A3DAC35B6FEF226 CRC64;

Query Match 10.1%; Score 128; DB 5; Length 1716;
 Best Local Similarity 21.4%; Pred. No. 0.083;

Matches 52; Conservative 50; Mismatches 85; Indels 56; Gaps 11;

QY 31 NRYTNVNDVTKLVAN-----LPKDYMTLKXVPGM-DVLPSCWISPMV---Q 76
 ID Q8MMW2 PRELIMINARY; PRT; 1716 AA.
 AC Q8MMW2 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Reticulocyte binding protein homolog 4.
 GN RH4.
 OS Plasmodium falciparum (isolate NF54).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NC NCB1_TaxID=5843;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22030722; PubMed=12034462;
 RA Kaneo O., Mu J.-B., Tsunboi T., Su X.-Z., Torii M.;
 RT "Gene structure and expression of a Plasmodium falciparum 220-kDa
 RT protein homologous to the Plasmodium vivax reticulocyte binding
 RT protein.";
 RL Mol. Biochem. Parasitol. 121:275-278 (2002).
 DR EMBL, AF432854; AAM47192.1; -
 SQ SEQUENCE 1716 AA; 205846 MW; 2A3DAC35B6FEF226 CRC64;

Query Match 10.1%; Score 128; DB 5; Length 1716;
 Best Local Similarity 21.4%; Pred. No. 0.083;

Matches 52; Conservative 50; Mismatches 85; Indels 56; Gaps 11;

QY 31 NRYTNVNDVTKLVAN-----LPKDYMTLKXVPGM-DVLPSCWISPMV---Q 76
 ID Q8MMW2 PRELIMINARY; PRT; 1716 AA.
 AC Q8MMW2 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Reticulocyte binding protein homolog 4.
 GN RH4.
 OS Plasmodium falciparum (isolate NF54).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NC NCB1_TaxID=5843;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22030722; PubMed=12034462;
 RA Kaneo O., Mu J.-B., Tsunboi T., Su X.-Z., Torii M.;
 RT "Gene structure and expression of a Plasmodium falciparum 220-kDa
 RT protein homologous to the Plasmodium vivax reticulocyte binding
 RT protein.";
 RL Mol. Biochem. Parasitol. 121:275-278 (2002).
 DR EMBL, AF432854; AAM47192.1; -
 SQ SEQUENCE 1716 AA; 205846 MW; 2A3DAC35B6FEF226 CRC64;

RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F27F5 from chromosome
1";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC007915; AAF69150.1; -
DR InterPro: IPR002713; FF.
DR InterPro: IPR001005; Myb DNA binding.
DR InterPro: IPR001202; WW_Reps_WWP.
DR Pfam: PF01846; FF; 5.
DR SMART: SM00397; WW; 2.
DR SMART: SM00441; FF; 4.
DR SMART: SM00456; WW; 2.
DR PROSITE: PS00037; MYB_1; 1.
DR PROSITE: PS50020; WW_DOMAIN_2; 2.
SQ SEQUENCE 937 AA; 107311 MW; 8c8fcd0641276a62 CRC64;

Query Match 8.6%; Score 109; DB 10; Length 937;
Best Local Similarity 24.5%; Pred. No. 1.5;
Matches 59; Conservative 31; Mismatches 99; Indels 52; Gaps 9;

QY 7 WILTCYLLLEPLVKTGICRNRYTNVNDVTK-LVANLEKDYITLKYPGMDVLP 65
DB 627 WLDYCTELK-----DLPQYQAVASNTSGSTPKDLFEDVTEELKQYHEKSYV----- 674
QY 66 SHCWISEMVVQLSDLTDLDFK-SNISEGLSNYSIID-KLVNIYDDLVCEVCKENSSKOL 123
DB 675 -----KDAKMSRKANFKSAISEDLSTQOISDINLKLIYDDLVGRVKEKEKEKA 722
QY 124 KKSFKSPERPLFTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKAKANPGDS 183
DB 723 RKLQRLAEF-----FTNLLHFKETITVASNMED-----SKLVESSQEVRSIGDE 767
QY 184 SLHWAMALALSLIIGFAFGALYMKKPSLTRAVENTQIENEDEISMLQEKEREFQ 243
DB 768 SVS-----OGLPEEYI-----TSIQEKAKERKRDKEKKEKRDKOKERR 817
QY 244 E 244
DB 818 E 818

RESULT 12
OSIM40
ID OSIM40 PRELIMINARY; PRT; 1515 AA.
AC OSIM40;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein, conserved.
OS Pf14_0051.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OC NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Paten A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Petrea M., Allen J., Selengut U., Haft D., Macher M.W., Valdivia A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA Mordred G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
falciparum";
RL Nature 419:498-511 (2002).
DR EMBL: AE014816; AAN36663.1; -
KW Hypothetical protein.
SQ SEQUENCE 1515 AA; 179830 MW; 6e5ea9823b80a006 CRC64;

Query Match 8.4%; Score 105.5; DB 5; Length 1515;
Best Local Similarity 21.3%; Pred. No. 5.5;
Matches 61; Conservative 48; Mismatches 101; Indels 77; Gaps 13;

QY 8 ILTCI-----YQLLEPLVKTGICRNRYTNVNDVTKLVANLPK-----DYMITLK 56
DB 685 VINCIRNRYDFSLVLSIFVNLN-----QNSFPLNIIKFEELMNIQIKMDNLDGLFSK 739
QY 57 YVPGMDVLT-----PSHCWISEMVV-----QLSDLTDLDFKPSNISEGLSNYSI 100
DB 740 FSYQSDIQAFNDPVIYHENDVNIINELKITEENKLEKSRDTLNTI-----ISNISE 793
QY 101 IKL-----VNIVDLVECVKENS KDLSKFSKSPERPLFTPEEFRIFNRSIDAFKDF 154
DB 794 CKTKRANRYDINLKLITIDNANDIIGIRKNIQKKKNNEQISDFPHLAKKSDVMKVL 853
QY 155 VVASETSDCVSSTLSPKAK-----NPQDSSLHWAMALPALFSLIIGF-AF 204
DB 854 YTDVQNKIKTYLFSIYKKKKINEIHNINIQSSVH-----ILSFVSNFLQIT 905
QY 205 GALT-----WKKOP-----SLTRAVENTQIENEDEISMLQEK 238
DB 906 QALYHTTNSLKKGS--LPICKHLISYENMSFNNIDKLAVIOCK 950

RESULT 13
ID Q9LPD8 PRELIMINARY; PRT; 919 AA.
AC Q9LPD8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE T12C22.20 protein.
GN T12C22.20.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Liu S., Vaysberg M., Sakano H., Lee J., Lenz C., Pham P., Toriumi M.,
RA Yu G., Chin C., Chou J., Choi E., Chung M., Gonzalez A., Hong B.,
RA Liu A., Alcafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.,
RA Hansen N., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
RA Nguyen M., Palm C., Shinn P., Southwick A., Davis R., Ecker J.,
RA Federspiel N., Theologis A.;
RT "The sequence of BAC T12C22 from Arabidopsis thaliana chromosome 1.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC020576; AAF78276.1; -
DR InterPro: IPR002713; FF.
DR InterPro: IPR001005; Myb DNA binding.
DR InterPro: IPR001202; WW_Reps_WWP.
DR Pfam: PF00397; WW; 4.
DR Pfam: PF01846; FF; 2.
DR SMART: SM00441; FF; 4.
DR SMART: SM00456; WW; 2.
DR PROSITE: PS00037; MYB_1; 1.
DR PROSITE: PS50020; WW_DOMAIN_2; 2.
SQ SEQUENCE 919 AA; 104903 MW; AF729850A28B661E CRC64;

Query Match 8.1%; Score 102.5; DB 10; Length 919;
Best Local Similarity 28.0%; Pred. No. 5.3;
Matches 49; Conservative 24; Mismatches 75; Indels 27; Gaps 6;

QY 72 EMVVOQSDLTDLDFK-SNISEGLSNYSIID-KLVNIYDDLVCEVCKENSSDKKFSK 129
DB 651 ELKQISWVSWLFEDFKSAISEDLSTQOISDINLKLIYDDLVGRVKEKEKEARLQRL 710
QY 130 PEPRFLTPEEFRIFNRSIDAFKDFVVASETSDCVSSTLSPKAKANPGDSLSHWMA 189

Db 711 ABE-----FTNLHTEKEITVASWED-----SKQVBESEQVRSIGDESVS--- 752
 QY 190 MALPALFSLIIGFAGALYKKRPSI/TRAVENTIOINEDNETISMLOEKEREPOE 244
 Db 753 ---QGLFEERY-----TSLOEKAKERKRDEKVRKREKDEKXKDKORRE 800

RESULT 14

Q96VK6 PRELIMINARY; PRT; 1498 AA.

AC Q96VK6; C1-DEC-2001 (Tremblrel. 19, Created)
 DT C1-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT C1-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE ABC transporter protein.
 GN ATRE.

OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; Emericella.
 OX NCB1_TaxID=162425;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=MG096;
 RA Andrade A.C., Braam C., Haas H., De Waard M.A.;
 RT "ABC transporters and resistance to azole fungicides in the ima
 mutants of Aspergillus nidulans."
 RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.

DR EMBL; AJ309280; CAC42216.1; -
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC_transporter.
 DR InterPro; IPR000847; HTH_LYR.
 DR Pfam; PF00005; ABC_tran; 2.
 DR ProDom; PD000006; ABC_transporter; 2.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
 DR PROSITE; PS00044; HTH_LYR_FAMILY; 1.
 DR PROSITE; PS00464; RIBOSOMAL_L22; 1.
 KW ATP-binding; Transport.
 SQ SEQUENCE 1498 AA; 167675 MW; BBE9FF3F46110FEB CRC64;

Query Match 8.1%; Score 102.5; DB 3; Length 1498;
 Best Local Similarity 19.6%; Pred. No. 9.7;
 Matches 56; Conservative 38; Mismatches 92; Indels 99; Gaps 10;

QY 17 LLENPLVKT-----EGICRNVYNNVQDYTKLVANLPKDYITLK---YVPG----- 60
 Db 263 LMFSLARAPRNRRLBEGVSRKQYAEHRDV--VMAMLGSHNTINRVGNDPIRGVSGGERK 320
 QY 61 -----MDVLPSCHWIS-----MVVQLSDSLTD 83
 Db 321 RVSIABEATLSQAPLQCMNDNSTRGLDSANALEFCCKNLALMSKTYGTACVAITYQASQAYD 380
 QY 84 LLDKFSNISGLSNY--SIIDKLVINIVDDIVECVKENSKDJKKFSPEPRLF----- 135
 Db 381 VEDKVTLYLEGROIYFGNTKDAKKPFVDMGFCPEPQRTADFLTSLTSPAERLVRPVEG 440
 QY 136 ----TPEEFRIFNRSIDAFK-----DFVVASETSDCVSSTLSPE-KGAKNPP 180
 Db 441 RVPCPTPEFAAMKRSEERAKLMAIEEYEROYPICGSPSYDAFVDARKAMQSKRQVNSP 500
 QY 181 -----GDSLHMAAMALPALFSLIIGFAF 204
 Db 501 YTISIMQOVSLCVVRGFORLGRDPSLTSTLIGNFMALITIGSVF 545

RESULT 15

Q9P884 PRELIMINARY; PRT; 1498 AA.

AC Q9P884; C1-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE ABC transporter protein.
 GN ATRE.
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; Emericella.
 OX NCB1_TaxID=162425;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MG096;
 RA Andrade A.C., Van Nistelrooy J.G.M., Haas H., De Waard M.A.;
 RT "ABC transporters and resistance to azole fungicides in the ima
 mutants of Aspergillus nidulans."
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL; AJ276241; CAB76823.1; -
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC_transporter.
 DR InterPro; IPR000847; HTH_LYR.
 DR Pfam; PF00005; ABC_tran; 2.
 DR ProDom; PD000006; ABC_transporter; 2.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
 DR PROSITE; PS00044; HTH_LYR_FAMILY; 1.
 DR PROSITE; PS00464; RIBOSOMAL_L22; 1.
 KW ATP-binding; Transport.
 SQ SEQUENCE 1498 AA; 167706 MW; AABDEA3FFD1ABREB CRC64;

Query Match 8.1%; Score 102.5; DB 3; Length 1498;
 Best Local Similarity 19.6%; Pred. No. 9.7;
 Matches 56; Conservative 38; Mismatches 92; Indels 99; Gaps 10;
 QY 17 LLENPLVKT-----EGICRNVYNNVQDYTKLVANLPKDYITLK---YVPG----- 60
 Db 263 LMFSLARAPRNRRLBEGVSRKQYAEHRDV--VMAMLGSHNTINRVGNDPIRGVSGGERK 320
 QY 61 -----MDVLPSCHWIS-----MVVQLSDSLTD 83
 Db 321 RVSIABEATLSQAPLQCMNDNSTRGLDSANALEFCCKNLALMSKTYGTACVAITYQASQAYD 380
 QY 84 LLDKFSNISGLSNY--SIIDKLVINIVDDIVECVKENSKDJKKFSPEPRLF----- 135
 Db 381 VEDKVTLYLEGROIYFGNTKDAKKPFVDMGFCPEPQRTADFLTSLTSPAERLVRPVEG 440
 QY 136 ----TPEEFRIFNRSIDAFK-----DFVVASETSDCVSSTLSPE-KGAKNPP 180
 Db 441 RVPCPTPEFAAMKRSEERAKLMAIEEYEROYPICGSPSYDAFVDARKAMQSKRQVNSP 500
 QY 181 -----GDSLHMAAMALPALFSLIIGFAF 204
 Db 501 YTISIMQOVSLCVVRGFORLGRDPSLTSTLIGNFMALITIGSVF 545

Search completed: February 5, 2004, 15:07:30
 Job time : 29.6846 secs